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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds
(without alignments)
65.338 Million cell updates/sec

Title: US-10-056-583A-64
Perfect score: 70
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	70	100.0	15	5	ABP52270	Abp52270 HLA-DR2 m
2	65	92.9	15	5	ABP52271	Abp52271 HLA-DR2 m
3	65	92.9	15	5	ABP52272	Abp52272 HLA-DR2 m
4	65	92.9	15	5	ABP52298	Abp52298 HLA-DR2 m
5	65	92.9	17	5	ABP52294	Abp52294 HLA-DR2 m
6	65	92.9	17	5	ABP52296	Abp52296 HLA-DR2 m
7	65	92.9	19	5	ABP52295	Abp52295 HLA-DR2 m
8	64	91.4	15	5	ABP52257	Abp52257 HLA-DR2 m
9	60	85.7	15	5	ABP52290	Abp52290 HLA-DR2 m
10	60	85.7	15	5	ABP52261	Abp52261 HLA-DR2 m
11	60	85.7	15	5	ABP52292	Abp52292 HLA-DR2 m
12	60	85.7	15	5	ABP52269	Abp52269 HLA-DR2 m
13	59	84.3	15	5	ABP52267	Abp52267 HLA-DR2 m
14	59	84.3	15	5	ABP52263	Abp52263 HLA-DR2 m
15	57	81.4	15	5	ABP52301	Abp52301 HLA-DR2 m
16	56	80.0	15	5	ABP52304	Abp52304 HLA-DR2 m
17	56	80.0	17	5	ABP52303	Abp52303 HLA-DR2 m
18	55	78.6	15	5	ABP52291	Abp52291 HLA-DR2 m
19	55	78.6	15	5	ABP52251	Abp52251 HLA-DR2 m
20	55	78.6	15	5	ABP52248	Abp52248 HLA-DR2 m
21	55	78.6	15	5	ABP52268	Abp52268 HLA-DR2 m
22	55	78.6	15	5	ABP52239	Abp52239 HLA-DR2 m
23	54.5	77.9	15	5	ABP52265	Abp52265 HLA-DR2 m
24	54	77.1	15	5	ABP52240	Abp52240 HLA-DR2 m
25	54	77.1	15	5	ABP52241	Abp52241 HLA-DR2 m

26	54	77.1	15	5	ABP52249	Abp52249 HLA-DR2 m
27	53	75.7	15	5	ABP52243	Abp52243 HLA-DR2 m
28	53	75.7	15	5	ABP52258	Abp52258 HLA-DR2 m
29	53	75.7	15	5	ABP52259	Abp52259 HLA-DR2 m
30	53	75.7	15	5	ABP52262	Abp52262 HLA-DR2 m
31	53	75.7	15	5	ABP52260	Abp52260 HLA-DR2 m
32	52	74.3	15	5	ABP52305	Abp52305 HLA-DR2 m
33	52	74.3	17	5	ABP52302	Abp52302 HLA-DR2 m
34	51	72.9	15	5	ABP52255	Abp52255 HLA-DR2 m
35	51	72.9	15	5	ABP52253	Abp52253 HLA-DR2 m
36	51	72.9	15	5	ABP52242	Abp52242 HLA-DR2 m
37	51	72.9	15	5	ABP52297	Abp52297 HLA-DR2 m
38	50	71.4	15	3	AAV58969	Aay58969 Copeptide
39	50	71.4	15	3	AAV82058	Aay82058 MHC class
40	50	71.4	15	4	AAG63198	Aag63198 Peptide w
41	50	71.4	15	5	ABP52256	Abp52256 HLA-DR2 m
42	50	71.4	15	5	ABP52289	Abp52289 HLA-DR2 m
43	50	71.4	15	5	ABP52266	Abp52266 HLA-DR2 m
44	50	71.4	15	7	ADJ57542	Adj57542 Cop-1 rel
45	50	71.4	15	8	ADQ59601	Adq59601 Copolymer

ALIGNMENTS

RESULT 1
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
AC ABP52270;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX

OS Homo sapiens.
OS Synthetic.

XX WO200259143-A2.

PN 01-AUG-2002.

PD 24-JAN-2002; 2002WO-US002071.

PR 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

XX Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (i) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 70; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAAKYEAYKAAAAA 15

RESULT 2
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
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PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
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XX encephalomyelitis.
PS Claim 28; Page 39; 54pp; English.
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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
XX invention
XX

SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00057;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAAKYEAYKAAAAA 15

RESULT 3
ABP52272
ID ABP52272 standard; peptide; 15 AA.
XX
AC ABP52272;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:66.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PS New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
XX demyelinating disease, e.g. multiple sclerosis, or post-viral
XX encephalomyelitis.
PS Claim 28; Page 39; 54pp; English.
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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
XX invention
XX
SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00057;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15

Db 1 EAKKYEAYKAAAAA 15

RESULT 4

ABP522298

ID ABP522298 standard; peptide; 15 AA.

XX AC ABP522298;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:92.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX KW immune response; antiinflammatory; neuroprotective; proliferation;

XX KW MHC class II protein inhibitor; demyelinating disease; inhibition;

XX KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 92.9%; Score 65; DB 5; Length 15;

Best Local Similarity 93.3%; Pred. No. 0.00057;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAAA 15

Db 1 EAKKYEAYKAAAAA 15

RESULT 5

ABP522294

ID ABP522294 standard; peptide; 17 AA.

XX ABP522294;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:88.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

XX KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

XX KW immune response; antiinflammatory; neuroprotective; proliferation;

XX KW MHC class II protein inhibitor; demyelinating disease; inhibition;

XX KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

XX KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.

OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 17 AA;

Query Match 92.9%; Score 65; DB 5; Length 17;

Best Local Similarity 93.3%; Pred. No. 0.00065;

Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAKKYEAYKAAAAA 15

Db 3 EAKKYEAYKAAAAA 17

RESULT 6

ABP522296

ID ABP522296 standard; peptide; 17 AA.

XX AC ABP522296;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:90.

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 OS
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PN 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 XX New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.
 XX
 PS Claim 28; Page 39; 54pp; English.
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 CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
 CC residues. The complex of the peptide with a major histocompatibility
 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
 CC immune response. (I) has antiinflammatory and neuroprotective activities,
 CC and can be used as a MHC class II protein inhibitor. The compositions
 CC comprising the peptides are useful for treating demyelinating diseases
 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 17 AA;
 Query Match 92.9%; Score 65; DB 5; Length 17;
 Best Local Similarity 93.3%; Pred. No. 0.00065;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EAAKYEAYKAAAAA 15
 Db 1 EKAKYEAYKAAAAA 15
 RESULT 7
 ABP52295
 ID ABP52295 standard; peptide; 19 AA.
 XX
 AC ABP52295;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:89.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PN 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 XX New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
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 PT encephalomyelitis.
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 CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
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 CC and can be used as a MHC class II protein inhibitor. The compositions
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 CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 19 AA;
 Query Match 92.9%; Score 65; DB 5; Length 19;
 Best Local Similarity 93.3%; Pred. No. 0.00073;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EAAKYEAYKAAAAA 15
 Db 3 EKAKYEAYKAAAAA 17
 RESULT 8
 ABP52257
 ID ABP52257 standard; peptide; 15 AA.
 XX
 AC ABP52257;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:51.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX

PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
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 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PS New compositions comprising synthetic peptides in complex with a major
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 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
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 PS Example 1; Page 32; 54pp; English.
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 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;
 Query Match 91.4%; Score 64; DB 5; Length 15;
 Best Local Similarity 93.3%; Pred. No. 0.0083;
 Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 EAAKYEAYKAAAAA 15
 Db ||||| ||||| ||||| ||||| |||||
 1 EAAKYAAYKAAAAA 15
 RESULT 9
 ABP52290
 ID ABP52290 standard; peptide; 15 AA.
 XX
 AC ABP52290;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:84.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.
 DR
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 CC demyelinating condition, and a side effect of administering an anti-
 CC tumour necrosis factor agents. The peptide further inhibits proliferation
 CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
 CC ABP52305 represent peptides used in the exemplification of the present
 CC invention
 XX
 SQ Sequence 15 AA;
 Query Match 85.7%; Score 60; DB 5; Length 15;
 Best Local Similarity 86.7%; Pred. No. 0.0037;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EAAKYEAYKAAAAA 15
 Db ||||| ||||| ||||| ||||| |||||
 1 EAPKYEAYKAAAAA 15
 RESULT 10
 ABP52261
 ID ABP52261 standard; peptide; 15 AA.
 XX
 AC ABP52261;
 XX
 DT 16-OCT-2002 (first entry)
 XX
 DE HLA-DR2 molecule binding peptide SEQ ID NO:55.
 XX
 KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
 KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
 KW immune response; antiinflammatory; neuroprotective; proliferation;
 KW MHC class II protein inhibitor; demyelinating disease; inhibition;
 KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
 KW anti-tumour necrosis factor agent.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200259143-A2.
 XX
 PD 01-AUG-2002.
 XX
 PF 24-JAN-2002; 2002WO-US002071.
 XX
 PR 24-JAN-2001; 2001US-0263569P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Strominger JL, Fridkis-Hareli M;
 XX
 DR WPI; 2002-608439/65.
 XX
 PT New compositions comprising synthetic peptides in complex with a major
 PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
 PT demyelinating disease, e.g. multiple sclerosis, or post-viral
 PT encephalomyelitis.

XX PS Example 1; Page 33; 54pp; English.

CC The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 85.7%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAAEYAYKAAAAA 15

RESULT 11

ABP52292

ID ABP52292 standard; peptide; 15 AA.

XX AC ABP52292;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:86.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.
OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.

XX PS New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

CC immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 85.7%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAPKYEAYKAAAAA 15

RESULT 12

ABP52269

ID ABP52269 standard; peptide; 15 AA.

XX AC ABP52269;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:63.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.
OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.

XX PS New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present invention

XX

SQ Sequence 15 AA;

Query Match 85.7%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
|||:|||||||

Db 1 EAAAYKAYKAAAAA 15

RESULT 13

ID ABP52267 standard; peptide; 15 AA.

XX

AC ABP52267;

XX

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:61.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

CC New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS Example 1; Page 33; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX

SQ Sequence 15 AA;

Query Match 84.3%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0055;

CC

XX

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
|||:|||||||

Db 1 EAKAYEAYKAAAAA 15

RESULT 14

ID ABP52263 standard; peptide; 15 AA.

XX

AC ABP52263;

XX

DT 16-OCT-2002 (first entry)

DE HLA-DR2 molecule binding peptide SEQ ID NO:57.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

CC New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS Example 1; Page 33; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX

SQ Sequence 15 AA;

Query Match 84.3%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0055;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
|||:|||||||

Db 1 EAKAYEAYKAAAAA 15

RESULT 15
ABP52301
ID ABP52301 standard; peptide; 15 AA.
XX
AC ABP52301;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:95.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 81.4%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.012;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EAAKYEAYKAAAAA 15
| | | | |
Db 1 EKAKFEAFKAAAAA 15

Search completed: March 31, 2005, 02:35:27
Job time : 89.7903 secs

;; APPLICANT: BRIGITTE DEVAUX
;; APPLICANT: JONATHAN B. ROTHBARD
;; APPLICANT: DAWN SMILEK
;; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE
;; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS
;; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE
;; NUMBER OF SEQUENCES: 95
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
;; STREET: 610 LINCOLN STREET
;; CITY: WALTHAM
;; STATE: Massachusetts
;; COUNTRY: USA
;; ZIP: 02145
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: ASCII text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US94/10257A
;; FILING DATE: 1 SEPTEMBER 1994
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/116,824
;; FILING DATE: 03-SEP-1993
;; CLASSIFICATION:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: ANNE I CRAIG
;; REGISTRATION NUMBER: 32,976
;; REFERENCE/DOCKET NUMBER: 071.1 PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 466-6000
;; TELEFAX: (617) 466-6040
;; INFORMATION FOR SEQ ID NO: 33:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 13 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
PCT-US94-10257A-33

Query Match 57.1%; Score 40; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 1.7;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AKYEAYKAAAAA 15
| | | | |
Db 1 AAYAAKAAAAA 13

RESULT 3
US-09-902-540-11110
; Sequence 11110, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11110
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11110

Query Match 57.1%; Score 40; DB 4; Length 391;
Best Local Similarity 53.3%; Pred. No. 59;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EAKYEAYKAAAAA 15
: | | | | | : |
Db 81 KAEAYRAYKASAGSA 95

RESULT 4
US-09-489-039A-13950
; Sequence 13950, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13950
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13950

Query Match 57.1%; Score 40; DB 4; Length 466;
Best Local Similarity 76.9%; Pred. No. 71;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AKYEAYKAAAAA 15
| | | | |
Db 153 ASLEAQKAAAAA 165

RESULT 5
US-07-988-754-4
; Sequence 4, Application US/07988754
; Patent No. 5374431
; GENERAL INFORMATION:
; APPLICANT: Pang, Roy H.L.
; APPLICANT: Cohen, Charles M.
; APPLICANT: Keck, Peter C.
; TITLE OF INVENTION: Synthetic Bioadhesive
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Creative Biomolecules
; STREET: 35 South Street
; CITY: Hopkinton
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,754
; FILING DATE: 19921210
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/627,323
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: CRP-046
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001


```

; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-07-988-754-4

Query Match          56.4%; Score 39.5; DB 1; Length 21;
Best Local Similarity 68.8%; Pred. No. 3.4;
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY      2 AAKYE---AYKAAAAA 14
      ||||: ||| ||||
Db      2 AAKYKAAAYKYAAAAA 17

RESULT 6
US-07-988-754-12
; Sequence 12, Application US/07988754
; Patent No. 5374431
; GENERAL INFORMATION:
; APPLICANT: Pang, Roy H.L.
; APPLICANT: Cohen, Charles M.
; APPLICANT: Keck, Peter C.
; TITLE OF INVENTION: Synthetic Bioadhesive
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Creative Biomolecules
; STREET: 35 South Street
; CITY: Hopkinton
; STATE: MA
; COUNTRY: U.S.A.
; ZIP: 01748
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/988,754
; FILING DATE: 19921210
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/627,323
; FILING DATE: 14-DEC-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Lunn, Paul G.
; REGISTRATION NUMBER: 32,743
; REFERENCE/DOCKET NUMBER: CRP-046
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (508) 435-9001
; TELEFAX: (508) 435-6951
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 33 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-988-754-12

Query Match          56.4%; Score 39.5; DB 1; Length 33;
Best Local Similarity 68.8%; Pred. No. 5.5;
Matches 11; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY      2 AAKYE---AYKAAAAA 14
      ||||: ||| ||||
Db      4 AAKYKAAAYKYAAAAA 19
```

```

RESULT 7
US-09-902-540-11242
; Sequence 11242, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 11242
; LENGTH: 186
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-11242

Query Match          55.7%; Score 39; DB 4; Length 186;
Best Local Similarity 61.5%; Pred. No. 40;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      2 AAKYEAYKAAAAA 14
      :||: ||||| |
Db      48 SASYQKYKAAADA 60

RESULT 8
US-08-836-620A-16
; Sequence 16, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORIGINAL SOURCE:
; ORGANISM: Rattus rattus
US-08-836-620A-16

Query Match          55.7%; Score 39; DB 2; Length 596;
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Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 56 EGAAYEFNAAAAA 70

RESULT 9
US-09-252-991A-21824
; Sequence 21824, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21824
; LENGTH: 601
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (601)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-21824

Query Match 55.7%; Score 39; DB 4; Length 601;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKYEAYKAAAAA 14
Db 570 ARYEAYRSAIVA 581

RESULT 10
US-09-252-991A-18769
; Sequence 18769, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18769
; LENGTH: 731
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18769

Query Match 55.7%; Score 39; DB 4; Length 731;
Best Local Similarity 72.7%; Pred. No. 1.7e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
Db 179 YEAYEACARA 189

RESULT 11
US-09-405-743A-6
; Sequence 6, Application US/09405743A
; Patent No. 6514938
; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A
; CURRENT APPLICATION NUMBER: US/09/405,743A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
US-09-405-743A-6

Query Match 55.0%; Score 38.5; DB 4; Length 86;
Best Local Similarity 73.3%; Pred. No. 22;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EAAKYEAYKAAAAA 15
Db 64 EAAK-KAYKAEAAKA 77

RESULT 12
US-09-816-989A-6
; Sequence 6, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6

Query Match 55.0%; Score 38.5; DB 4; Length 86;
Best Local Similarity 73.3%; Pred. No. 22;
Matches 11; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 1 EAAKYEAYKAAAAA 15
Db 64 EAAK-KAYKAEAAKA 77

RESULT 13
US-09-248-796A-26627
; Sequence 26627, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS

; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 26627

; LENGTH: 64

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-26627

Query Match 54.3%; Score 38; DB 4; Length 64;

Best Local Similarity 71.4%; Pred. No. 19;

Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AAKYEAYKAAAAA 15

|| || || || || || || ||

Db 48 AAAAAAYAAAAAA 61

RESULT 14

US-09-252-991A-29581

; Sequence 29581, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 29581

; LENGTH: 407

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-29581

Query Match 54.3%; Score 38; DB 4; Length 407;

Best Local Similarity 71.4%; Pred. No. 1.3e+02;

Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAKYEAYKAAAAA 14

||||| : | |||||

Db 263 EAKKKKAAAAAAA 276

RESULT 15

US-09-252-991A-32086

; Sequence 32086, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074,788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094,190

; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 32086

; LENGTH: 534

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-32086

Query Match 54.3%; Score 38; DB 4; Length 534;

Best Local Similarity 64.3%; Pred. No. 1.7e+02;

Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14

||||| : | |||||

Db 332 EAAHVEAHRADAAA 345

Search completed: March 31, 2005, 02:44:07

Job time : 22.9839 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds
(without alignments)
74.648 Million cell updates/sec

Title: US-10-056-583A-64
Perfect score: 70
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	70	100.0	15	14	US-10-056-583-64
2	65	92.9	15	14	US-10-056-583-65
3	65	92.9	15	14	US-10-056-583-66
4	65	92.9	17	14	US-10-056-583-88
5	65	92.9	17	14	US-10-056-583-90
6	65	92.9	19	14	US-10-056-583-89
7	64	91.4	15	14	US-10-056-583-51
8	60	85.7	15	14	US-10-056-583-55
9	60	85.7	15	14	US-10-056-583-63
10	60	85.7	15	14	US-10-056-583-84
11	60	85.7	15	14	US-10-056-583-86
12	59	84.3	15	14	US-10-056-583-57
13	59	84.3	15	14	US-10-056-583-61

14	57	81.4	15	14	US-10-056-583-95	Sequence 95, Appl
15	56	80.0	15	14	US-10-056-583-92	Sequence 92, Appl
16	56	80.0	15	14	US-10-056-583-98	Sequence 98, Appl
17	56	80.0	17	14	US-10-056-583-97	Sequence 97, Appl
18	55	78.6	15	14	US-10-056-583-33	Sequence 33, Appl
19	55	78.6	15	14	US-10-056-583-42	Sequence 42, Appl
20	55	78.6	15	14	US-10-056-583-45	Sequence 45, Appl
21	55	78.6	15	14	US-10-056-583-62	Sequence 62, Appl
22	55	78.6	15	14	US-10-056-583-85	Sequence 85, Appl
23	54.5	77.9	15	14	US-10-056-583-59	Sequence 59, Appl
24	54	77.1	15	14	US-10-056-583-34	Sequence 34, Appl
25	54	77.1	15	14	US-10-056-583-35	Sequence 35, Appl
26	54	77.1	15	14	US-10-056-583-43	Sequence 43, Appl
27	53	75.7	15	14	US-10-056-583-37	Sequence 37, Appl
28	53	75.7	15	14	US-10-056-583-52	Sequence 52, Appl
29	53	75.7	15	14	US-10-056-583-53	Sequence 53, Appl
30	53	75.7	15	14	US-10-056-583-54	Sequence 54, Appl
31	53	75.7	15	14	US-10-056-583-56	Sequence 56, Appl
32	52	74.3	15	14	US-10-056-583-99	Sequence 99, Appl
33	52	74.3	17	14	US-10-056-583-96	Sequence 96, Appl
34	51	72.9	15	14	US-10-056-583-36	Sequence 36, Appl
35	51	72.9	15	14	US-10-056-583-47	Sequence 47, Appl
36	51	72.9	15	14	US-10-056-583-49	Sequence 49, Appl
37	51	72.9	15	14	US-10-056-583-91	Sequence 91, Appl
38	50	71.4	15	9	US-09-765-301-24	Sequence 24, Appl
39	50	71.4	15	10	US-09-765-644A-24	Sequence 24, Appl
40	50	71.4	15	14	US-10-056-583-50	Sequence 50, Appl
41	50	71.4	15	14	US-10-056-583-60	Sequence 60, Appl
42	50	71.4	15	14	US-10-056-583-83	Sequence 83, Appl
43	50	71.4	15	15	US-10-438-538-28	Sequence 28, Appl
44	49	70.0	15	14	US-10-056-583-26	Sequence 26, Appl
45	49	70.0	15	14	US-10-056-583-30	Sequence 30, Appl

ALIGNMENTS

RESULT 1
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

Query Match 100.0%; Score 70; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 9e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
| | | | | | | | | | | | | | |
Db 1 EAAKYEAYKAAAAA 15

RESULT 2
US-10-056-583-65

```
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match          92.9%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EAAKYEAYKAAAAA 15
Db 1 EKAKYEAYKAAAAA 15
```

```
RESULT 3
US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66
```

```
Query Match          92.9%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00058;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EAAKYEAYKAAAAA 15
Db 1 EKAKYEAYKAAAAA 15
```

```
RESULT 4
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
```

```
Query Match          92.9%; Score 65; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EAAKYEAYKAAAAA 15
Db 3 EKAKYEAYKAAAAA 17
```

```
RESULT 5
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match          92.9%; Score 65; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.00066;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 EAAKYEAYKAAAAA 15
Db 1 EKAKYEAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```



```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569.
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

```
Query Match          92.9%; Score 65; DB 14; Length 19;
Best Local Similarity 93.3%; Pred. No. 0.00074;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAAKYEAYKAAAAA 15
        | ||||| |||||
Db       3 EKAKYEAYKAAAAA 17
```

```
RESULT 7
US-10-056-583-51
; Sequence 51, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51
```

```
Query Match          91.4%; Score 64; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00084;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAAKYEAYKAAAAA 15
        | ||||| |||||
Db       1 EAAKYAAYKAAAAA 15
```

```
RESULT 8
US-10-056-583-55
; Sequence 55, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 55
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-55
```

```
Query Match          85.7%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAAKYEAYKAAAAA 15
        | ||||| |||||
Db       1 EAAEYAAAYKAAAAA 15
```

```
RESULT 9
US-10-056-583-63
; Sequence 63, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 63
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-63
```

```
Query Match          85.7%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EAAKYEAYKAAAAA 15
        | ||||| |||||
Db       1 EAAAYKAYKAAAAA 15
```

```
RESULT 10
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match      85.7%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAPKYEAYKAAAAA 15

RESULT 11
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match      85.7%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0037;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAPKYEAYKAAAAA 15

RESULT 12
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57

Query Match      84.3%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAPKYEAYKAAAAA 15

RESULT 13
US-10-056-583-61
; Sequence 61, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 61
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-61

Query Match      84.3%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0054;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EAPKYEAYKAAAAA 15

RESULT 14
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match      81.4%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.011;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
Db 1 EKAKFEAFKAAAAA 15
```

RESULT 15
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

Query Match 80.0%; Score 56; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.016;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
| | | | |
Db 1 EKAKKEAYKAAAAA 15

Search completed: March 31, 2005, 02:48:48
Job time : 67.5323 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds
(without alignments)
80.614 Million cell updates/sec

Title: US-10-056-583A-64
Perfect score: 70
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	42	60.0	188	2	I50145	homeotic protein H
2	42	60.0	254	2	H86355	probable 14-3-3 pr
3	42	60.0	289	2	A43562	homeotic protein H
4	42	60.0	527	2	E69351	phosphoglycerate d
5	41	58.6	124	2	E84764	hypothetical prote
6	41	58.6	1857	1	S01787	fatty-acid synthas
7	41	58.6	2129	2	T27431	hypothetical prote
8	40	57.1	251	2	C70521	1-acylglycerol-3-p
9	40	57.1	354	1	GNVVS	genome polyprotein
10	40	57.1	788	2	F97547	probable oxidoredu
11	40	57.1	788	2	AC2767	formate dehydrogen
12	40	57.1	806	2	T13690	hypothetical prote
13	40	57.1	1151	2	T18535	high molecular mas
14	39	55.7	101	2	G75512	conserved hypothet
15	39	55.7	170	2	E81312	probable lipoprote
16	39	55.7	250	2	T51971	proteasome endopep
17	39	55.7	519	2	S39893	rnfc protein - Rho
18	39	55.7	553	2	D83640	hypothetical prote
19	39	55.7	599	1	QRMSE	estrogen receptor
20	39	55.7	600	1	QRRTE	estrogen receptor
21	39	55.7	698	2	T32594	hypothetical prote
22	39	55.7	728	2	H82965	DNA helicase II PA
23	38	54.3	108	2	F97521	VCO33 protein homo
24	38	54.3	108	2	AH2740	conserved hypothet
25	38	54.3	261	2	T51222	hypothetical prote
26	38	54.3	331	1	DEECG3	glyceraldehyde-3-p
27	38	54.3	331	2	AG0711	glyceraldehyde-3-p
28	38	54.3	331	2	D85788	glyceraldehyde-3-p
29	38	54.3	331	2	H90939	glyceraldehyde-3-p

30	54.3	38	54.3	346	2	C82156	conserved hypothet
31	54.3	38	54.3	347	2	E83525	TolA protein PA097
32	54.3	38	54.3	377	2	T43037	probable fatty-aci
33	54.3	38	54.3	424	2	B81936	tetrahydrofolylpol
34	54.3	38	54.3	424	2	C81170	folylpolyglutamate
35	54.3	38	54.3	428	2	E87463	hypothetical prote
36	54.3	38	54.3	433	2	D87408	ATPase, AAA family
37	54.3	38	54.3	478	2	S04675	H+-transporting tw
38	54.3	38	54.3	478	2	E87470	efflux system prot
39	54.3	38	54.3	521	2	T49355	related to protein
40	54.3	38	54.3	1842	2	T43409	probable fatty-aci
41	54.3	38	54.3	1842	2	T38781	fatty acid synthas
42	52.9	37	52.9	165	2	B87702	ribosomal protein
43	52.9	37	52.9	176	2	G87606	transcription regu
44	52.9	37	52.9	185	2	S36290	T-cell receptor ga
45	52.9	37	52.9	189	2	S77930	exoskeletal protei

ALIGNMENTS

RESULT 1

I50145
homeotic protein Hox M - chicken
N;Alternate names: CHOX M
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: I50145; S14512
R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A;Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic vir
A;Reference number: I50145; MUID:91238215; PMID:1674560
A;Accession: I50145
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-188 <CRO>
A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:G62700; PIDN:CAA0445.1; PID:G62701
C;Genetics:
A;Gene: CHOX M
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;96-152/Domain: homeobox homology <HOX>

Query Match 60.0%; Score 42; DB 2; Length 188;
Best Local Similarity 81.8%; Pred. No. 9.8;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
| |||||
Db 10 YSKYKAAAAA 20

RESULT 2

H86355
probable 14-3-3 protein T16E15.8 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86355
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86355
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-254 <STO>

A;Cross-references: UNIPROT:P48347; GB:AE005172; NID:g9392684; PIDN:AAF87261.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: 14-3-3 protein

Query Match 60.0%; Score 42; DB 2; Length 254;
Best Local Similarity 70.6%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EAA--KYEAYKAAAAA 15
||| ||||| |||
Db 144 EAADQSLEAYKAAVAAA 160

RESULT 3
A43562
homeotic protein Hox D8 - mouse
N;Alternate names: homeotic protein Hox 4.3
C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou
Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob
A;Reference number: A43562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-289 <IZP>
A;Cross-references: UNIPROT:P23463
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>

Query Match 60.0%; Score 42; DB 2; Length 289;
Best Local Similarity 81.8%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
| ||||| |||
Db 10 YSKYKAAAAA 20

RESULT 4
E69351
phosphoglycerate dehydrogenase (serA) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69351
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69351
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-527 <KLE>
A;Cross-references: UNIPROT:O29445; GB:AE001048; GB:AE000782; NID:g2689371; PIDN:AAB9042
C;Superfamily: Bacillus phosphoglycerate dehydrogenase

Query Match 60.0%; Score 42; DB 2; Length 527;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
||| ||| |||
Db 236 EAALYEAIKAGKVA 250

A;Cross-references: UNIPROT:P48347; GB:AE005172; NID:g9392684; PIDN:AAF87261.1; GSPDB:GN
C;Genetics:
A;Map position: 1
C;Superfamily: 14-3-3 protein

Query Match 60.0%; Score 42; DB 2; Length 254;
Best Local Similarity 70.6%; Pred. No. 13;
Matches 12; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 EAA--KYEAYKAAAAA 15
||| ||||| |||
Db 144 EAADQSLEAYKAAVAAA 160

RESULT 3
A43562
homeotic protein Hox D8 - mouse
N;Alternate names: homeotic protein Hox 4.3
C;Species: Mus musculus (house mouse)
C;Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43562
R;Izpisua-Belmonte, J.C.; Dolle, P.; Renucci, A.; Zappavigna, V.; Falkenstein, H.; Dubou
Development 110, 733-745, 1990
A;Title: Primary structure and embryonic expression pattern of the mouse Hox-4.3 homeob
A;Reference number: A43562; MUID:91209232; PMID:1982431
A;Accession: A43562
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-289 <IZP>
A;Cross-references: UNIPROT:P23463
C;Superfamily: homeotic protein Hox A7; homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;196-252/Domain: homeobox homology <HOX>

Query Match 60.0%; Score 42; DB 2; Length 289;
Best Local Similarity 81.8%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 YEAYKAAAAA 15
| ||||| |||
Db 10 YSKYKAAAAA 20

RESULT 4
E69351
phosphoglycerate dehydrogenase (serA) homolog - Archaeoglobus fulgidus
C;Species: Archaeoglobus fulgidus
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C;Accession: E69351
R;Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.
Nature 390, 364-370, 1997
A;Authors: Utterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.; Sykes, S.
Smith, H.O.; Woese, C.R.; Venter, J.C.
A;Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo
A;Reference number: A69250; MUID:98049343; PMID:9389475
A;Accession: E69351
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-527 <KLE>
A;Cross-references: UNIPROT:O29445; GB:AE001048; GB:AE000782; NID:g2689371; PIDN:AAB9042
C;Superfamily: Bacillus phosphoglycerate dehydrogenase

Query Match 60.0%; Score 42; DB 2; Length 527;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 10; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
||| ||| |||
Db 236 EAALYEAIKAGKVA 250

RESULT 5
E84764

hypothetical protein At2g35090 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004

C;Accession: E84764

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: E84764

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-124 <STO>

A;Cross-references: UNIPROT:O82182; GB:AE002093; NID:g3668094; PIDN:AAC61826.1; GSPDB:GN

C;Genetics:

A;Gene: At2g35090

A;Map position: 2

Query Match 58.6%; Score 41; DB 2; Length 124;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 9; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15

||| ||| ||| |||

Db 99 EAVKYAAYTLVAVAA 113

RESULT 6

S01787

fatty-acid synthase (EC 2.3.1.85) - Penicillium griseofulvum

N;Alternate names: fatty acid synthetase

C;Species: Penicillium griseofulvum

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: S01787

R;Wiesner, P.; Beck, J.; Beck, K.F.; Ripka, S.; Mueller, G.; Luecke, S.; Schweizer, E.

Eur. J. Biochem. 177, 69-79, 1988

A;Title: Isolation and sequence analysis of the fatty acid synthetase PAS2 gene from Peni

A;Reference number: S01787; MUID:89030697; PMID:3053172

A;Accession: S01787

A;Status: not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-1857 <WIE>

A;Cross-references: UNIPROT:P15368; GB:M37461; NID:g169179; PIDN:AAA33695.1; PID:g169180

A;Note: the source is designated as Penicillium patulum

C;Genetics:

A;Gene: fas2

C;Superfamily: yeast fatty-acid synthase

C;Keywords: acyltransferase; coenzyme A

Query Match 58.6%; Score 41; DB 1; Length 1857;

Best Local Similarity 66.7%; Pred. No. 1.2e+02;

Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAKYEAYKAAAA 13

|:||||| |||:

Db 62 ASKYEAYDAATS 73

RESULT 7

T27431

hypothetical protein Y79H2A.3 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C;Accession: T27431

R;Matthews, L.

submitted to the EMBL Data Library, September 1999

A;Reference number: Z20365

A;Accession: T27431

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-2129 <WIL>
A;Cross-references: UNIPROT:Q9U1R8; EMBL:AL110501; NID:e1542357; PIDN:CAB54509.1; CESP:Y
A;Experimental source: clone Y79H2A
C;Genetics:
A;Gene: CESP:Y79H2A.3
A;Introns: 39/3; 75/1; 125/3; 212/3; 254/1; 330/3; 460/1; 486/3; 540/3; 580/3; 631/1; 67
; 1760/1; 1929/3; 2037/3; 2074/3

Query Match 58.6%; Score 41; DB 2; Length 2129;
Best Local Similarity 56.7%; Pred. No. 1.4e+02;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAA 12
| | | | | : : : |
Db 144 EYAKYERYRSAA 155

RESULT 8
C70521
1-acylglycerol-3-phosphate O-acyltransferase (EC 2.3.1.51) homolog - Mycobacterium tuber
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 16-Aug-2004
C;Accession: C70521
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: C70521
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-251 <COL>
A;Cross-references: UNIPROT:O07808; GB:Z97188; GB:AL123456; NID:g3261805; PIDN:CAB10008.
A;Experimental source: strain H37Rv
C;Genetics:
A;Gene: RV3815C
C;Superfamily: 1-acyl-sn-glycerol-3-phosphate acyltransferase
C;Keywords: acyltransferase; coenzyme A

Query Match 57.1%; Score 40; DB 2; Length 251;
Best Local Similarity 56.7%; Pred. No. 27;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAA 15
| | | | | : : : |
Db 229 EAARMEADEAARAA 243

RESULT 9
GNVUSR
genome polyprotein 1 - tomato ringspot virus (strain raspberry) (fragment)
C;Species: tomato ringspot virus
C;Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004
C;Accession: A40787
R;Rott, M.E.; Tremaine, J.H.; Rochon, D.M.
Virology 185, 468-472, 1991
A;Title: Comparison of the 5' and 3' termini of tomato ringspot virus RNA1 and RNA2: evi
A;Reference number: A40787; MUID:92024112; PMID:1926788
A;Accession: A40787
A;Molecule type: genomic RNA
A;Residues: 1-354 <ROT>
A;Cross-references: UNIPROT:P29150; GB:M73822; NID:g335267; PIDN:AAA47941.1; PID:g5555406
C;Genetics:
A;Map position: segment 1
C;Superfamily: tomato ringspot virus genome polyprotein
C;Keywords: glycoprotein; polyprotein
F;270/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 57.1%; Score 40; DB 1; Length 354;
Best Local Similarity 57.9%; Pred. No. 38;
Matches 11; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 1 EAAKYEAY-----KAAAAA 15
: | | | | | : | | | | |
Db 182 KAAKYAAFAARKKAAAVAA 200

RESULT 10
F97547
probable oxidoreductase (PA5181) [imported] - Agrobacterium tumefaciens (strain C58, Cer
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97547
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tur
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97547
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-788 <KUR>
A;Cross-references: UNIPROT:Q8UF51; GB:AE007869; PIDN:AAK87335.1; PID:gl15156635; GSPDB:B
C;Genetics:
A;Gene: AGR_C.2854
A;Map position: circular chromosome
C;Superfamily: formate dehydrogenase

Query Match 57.1%; Score 40; DB 2; Length 788;
Best Local Similarity 61.5%; Pred. No. 80;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAKYEAYKAAAA 14
| | | | | : : : |
Db 343 AAEFEAYRAAVDA 355

RESULT 11
AC2767
formate dehydrogenase H alpha subunit fdhF [imported] - Agrobacterium tumefaciens (stra
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AC2767
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenthner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AC2767
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-788 <KUR>
A;Cross-references: UNIPROT:Q8UF51; GB:AE008688; PIDN:AAL42553.1; PID:gl7739976; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: fdhF
C;Map position: circular chromosome
C;Superfamily: formate dehydrogenase

Query Match 57.1%; Score 40; DB 2; Length 788;
Best Local Similarity 61.5%; Pred. No. 80;
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAKYEAYKAAAA 14
| | | | | : : : |
Db 343 AAEFEAYRAAVDA 355

RESULT 12
T13690
hypothetical protein EG0003.2 - fruit fly (Drosophila melanogaster)

```

C:Species: Drosophila melanogaster
C>Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 09-Jul-2004
C:Accession: T13690
R:Murphy, L.; Harris, D.; Barrell, B.
submitted to the EMBL Data Library, November 1998
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.
A:Reference number: Z17699
A:Accession: T13690
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-806 <MUR>
A:Cross-references: UNIPROT:O96828; EMBL:AL031863; NID:e1331652; PID:e1355938; PIDN:CAA21
C:Genetics:
A:Cross-references: FlyBase:FBgn0025833
A:Introns: 37/3; 448/3; 611/2; 690/3
A>Note: EG:EG0003.2

Query Match      57.1%; Score 40; DB 2; Length 806;
Best Local Similarity 69.2%; Pred. No. 82;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 AKYEAYKAAAAA 15
Db      743 AQYSQYYAAAAA 755
      |:| | | | | | |
      |:| | | | | | |

RESULT 13
T18535
high molecular mass nuclear antigen - chicken (fragment)
C:Species: Gallus gallus (chicken)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T18535
R:Shimada, K.; Harata, M.; Mizuno, S.
J. Cell Sci. 110, 3031-3041, 1997
A:Title: A nuclear matrix-associated high molecular mass nuclear antigen, HMNA, of chicken
A:Reference number: Z18955; MUID:9803440; PMID:9365273
A:Accession: T18535
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-1151 <SHI>
A:Cross-references: UNIPROT:O57580; EMBL:D88440; NID:d1177138; PID:d1025045; PIDN:BAA241

Query Match      57.1%; Score 40; DB 2; Length 1151;
Best Local Similarity 73.3%; Pred. No. 1.1e+02;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      1 EAAKYEAYKAAAAA 15
Db      1100 EAAVQEAATAAAAAA 1114
      ||| || | | | | |
      ||| || | | | | |

RESULT 14
G75512
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: G75512
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: G75512
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-101 <WHI>
A:Cross-references: UNIPROT:Q9RX23; GB:AE001908; GB:AE000513; NID:g6458174; PIDN:AAF1006
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR0492
A:Map position: 1

```

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds
(without alignments)
95.342 Million cell updates/sec

Title: US-10-056-583A-64
Perfect score: 70
Sequence: 1 EAAKYEAYKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	65.7	847	2	Q7SC23
2	45	64.3	603	2	Q64JV8
3	45	64.3	608	2	Q64JV9
4	45	64.3	608	2	Q64JW1
5	45	64.3	614	2	Q64JV2
6	45	64.3	727	2	Q64JU8
7	45	64.3	727	2	Q64JV3
8	45	64.3	727	2	Q64JV7
9	45	64.3	810	2	Q64JV4
10	45	64.3	826	2	Q64JW3
11	45	64.3	897	2	Q64JW5
12	45	64.3	900	2	Q64JW4
13	45	64.3	927	2	Q64JV1
14	44	62.9	501	2	Q6DLT8
15	44	62.9	509	2	Q6DLT7
16	44	62.9	525	2	Q6DLT9
17	44	62.9	530	2	Q6DLU0
18	44	62.9	705	2	Q64JV5
19	44	62.9	2058	2	Q6DLT4
20	44	62.9	2064	2	Q6DLT3
21	43	61.4	188	2	Q72BU7
22	43	61.4	395	2	Q6D7F3
23	42	60.0	188	1	HXD8 CHICK
24	42	60.0	206	2	Q87SY7
25	42	60.0	254	1	143A ARATH
26	42	60.0	277	2	Q6ATQ0
27	42	60.0	289	1	HXD8 MOUSE
28	42	60.0	289	2	Q8IXZ1
29	42	60.0	290	1	HXD8 HUMAN
30	42	60.0	342	2	Q6ATQ1
31	42	60.0	380	2	Q8W0D1

32	42	60.0	390	2	Q6I5H3	Q6I5H3 oryza sativ
33	42	60.0	527	1	SERA_ARCFU	Q29445 archaeoglob
34	42	60.0	608	2	Q64JV6	Q64JV6 plasmodium
35	42	60.0	697	2	Q9NDJ0	Q9NDJ0 plasmodium
36	42	60.0	697	2	Q64JW6	Q64JW6 plasmodium
37	42	60.0	853	2	Q7S637	Q7S637 neurospora
38	41	58.6	99	1	CU02_BLACR	P80676 blaberus cr
39	41	58.6	124	2	O82182	O82182 arabidopsis
40	41	58.6	216	2	Q95V10	Q95V10 fasciola he
41	41	58.6	415	2	Q6YWS1	Q6YWS1 oryza sativ
42	41	58.6	432	2	Q8IRS8	Q8IRS8 drosophila
43	41	58.6	453	2	Q6AV91	Q6AV91 oryza sativ
44	41	58.6	508	2	Q6QUT5	Q6QUT5 corynebacte
45	41	58.6	512	2	Q7XVB8	Q7XVB8 oryza sativ

ALIGNMENTS

RESULT 1
Q7SC23
ID Q7SC23 PRELIMINARY; PRT; 847 AA.
AC Q7SC23;
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU08397.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseles M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbola D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DDBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000143; EAA34000.1; -.
DR InterPro; IPR004648; Oligopept_transpt.
DR InterPro; IPR004813; Tetrapept_transpt.
DR Pfam; PF03169; OPT; 1.
DR TIGRFAMs; TIGR00727; ISP4_OPT; 1.
DR TIGRFAMs; TIGR00728; OPT_5fam; 1.
KW Hypothetical protein.
SQ SEQUENCE 847 AA; 94963 MW; CDAF7C5D5EFD910A CRC64;

Query Match 65.7%; Score 46; DB 2; Length 847;
Best Local Similarity 66.7%; Pred. No. 56;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 15
:|||||||
Db 462 DAAKYEAYSPAYLAA 476

RESULT 2

Q64JV8
ID Q64JV8 PRELIMINARY; PRT; 603 AA.
AC Q64JV8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br781B;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454088; AAS10474.1; --
KW Merozoite.
FT NON_TER 1 1
FT NON_TER 603 603
SQ SEQUENCE 603 AA; 65111 MW; 9FB464A42ED295C4 CRC64;
Query Match 64.3%; Score 45; DB 2; Length 603;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EAAKYEAYKAAAAA 14
Db 398 EAAKEEAQKAATAA 411
RESULT 3
Q64JV9
ID Q64JV9 PRELIMINARY; PRT; 608 AA.
AC Q64JV9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br67T;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454087; AAS10473.1; --
KW Merozoite.
FT NON_TER 1 1
FT NON_TER 608 608
SQ SEQUENCE 608 AA; 65834 MW; FEC7E2627E333604 CRC64;
Query Match 64.3%; Score 45; DB 2; Length 608;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EAAKYEAYKAAAAA 14
Db 403 EAAKEEAQKAATAA 416
RESULT 4
Q64JW1
ID Q64JW1 PRELIMINARY; PRT; 608 AA.
AC Q64JW1;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br56;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454085; AAS10471.1; --
KW Merozoite.
FT NON_TER 1 1
FT NON_TER 608 608
SQ SEQUENCE 608 AA; 65845 MW; A07CDB0563F4FE03 CRC64;
Query Match 64.3%; Score 45; DB 2; Length 608;
Best Local Similarity 78.6%; Pred. No. 60;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EAAKYEAYKAAAAA 14
Db 403 EAAKEEAQKAATAA 416
RESULT 5
Q64JV2
ID Q64JV2 PRELIMINARY; PRT; 614 AA.
AC Q64JV2;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ong;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454094; AAS10480.1; --
KW Merozoite.
FT NON_TER 1 1
FT NON_TER 614 614
SQ SEQUENCE 614 AA; 66444 MW; 2C5C5B13F2FCBCA9 CRC64;
Query Match 64.3%; Score 45; DB 2; Length 614;
Best Local Similarity 78.6%; Pred. No. 61;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 EAAKYEAYKAAAAA 14
Db 409 EAAKEEAQKAATAA 422
RESULT 6
Q64JU8
ID Q64JU8 PRELIMINARY; PRT; 727 AA.
AC Q64JU8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

```
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Thai;
RX PubMed=15374528;
RA Barnwell J.W.;
RA "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454098; AAS10484.1; -.
KW Merozoite.
FT NON_TER 1 727
FT SEQUENCE 727 AA; 78545 MW; EAD28262EF32531B CRC64;
SQ

Query Match 64.3%; Score 45; DB 2; Length 727;
Best Local Similarity 78.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
   ||||| |||||
Db 522 EAAKEEAQKAATAA 535

RESULT 7
Q64JV3 ID Q64JV3 PRELIMINARY; PRT; 727 AA.
AC Q64JV3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NK;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454093; AAS10479.1; -.
KW Merozoite.
FT NON_TER 1 727
FT SEQUENCE 727 AA; 78556 MW; B3A309A6874F5B0D CRC64;
SQ

Query Match 64.3%; Score 45; DB 2; Length 727;
Best Local Similarity 78.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
   ||||| |||||
Db 522 EAAKEEAQKAATAA 535

RESULT 8
Q64JV7 ID Q64JV7 PRELIMINARY; PRT; 727 AA.
AC Q64JV7;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br781T;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454089; AAS10475.1; -.
KW Merozoite.
FT NON_TER 1 727
FT SEQUENCE 727 AA; 78668 MW; F1D764F1BB782E5C CRC64;
SQ

Query Match 64.3%; Score 45; DB 2; Length 727;
Best Local Similarity 78.6%; Pred. No. 71;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
   ||||| |||||
Db 522 EAAKEEAQKAATAA 535

RESULT 9
Q64JV4 ID Q64JV4 PRELIMINARY; PRT; 810 AA.
AC Q64JV4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454092; AAS10478.1; -.
KW Merozoite.
FT NON_TER 1 810
FT SEQUENCE 810 AA; 86539 MW; 14B1E39FAE44F74A CRC64;
SQ

Query Match 64.3%; Score 45; DB 2; Length 810;
Best Local Similarity 78.6%; Pred. No. 78;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
   ||||| |||||
Db 605 EAAKEEAQKAATAA 618

RESULT 10
Q64JW3 ID Q64JW3 PRELIMINARY; PRT; 826 AA.
AC Q64JW3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
```

```
RC STRAIN=Chess;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454083; AAS10469.1; -.
KW Merozoite.
FT NON TER 826 826
SQ SEQUENCE 826 AA; 89752 MW; 699B1F21F5B747B6 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 826;
Best Local Similarity 78.6%; Pred. No. 80;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 572 EAAKEEAQKAATAA 585

RESULT 11
Q64JW5 ID Q64JW5 PRELIMINARY; PRT; 897 AA.
AC Q64JW5;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br1T;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454081; AAS10467.1; -.
KW Merozoite.
FT NON TER 897 897
SQ SEQUENCE 897 AA; 96705 MW; CB86BFC3CBED5EA CRC64;

Query Match 64.3%; Score 45; DB 2; Length 897;
Best Local Similarity 78.6%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 643 EAAKEEAQKAATAA 656

RESULT 12
Q64JW4 ID Q64JW4 PRELIMINARY; PRT; 900 AA.
AC Q64JW4;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Br69;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
```

```
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454082; AAS10468.1; -.
KW Merozoite.
FT NON TER 900 900
SQ SEQUENCE 900 AA; 97231 MW; DC84487C0D34BF7B CRC64;

Query Match 64.3%; Score 45; DB 2; Length 900;
Best Local Similarity 78.6%; Pred. No. 86;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 646 EAAKEEAQKAATAA 659

RESULT 13
Q64JV1 ID Q64JV1 PRELIMINARY; PRT; 927 AA.
AC Q64JV1;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Merozoite surface protein 3b (Fragment).
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sal1;
RX PubMed=15374528;
RA Rayner J.C., Huber C.S., Feldman D., Ingravallo P., Galinski M.R.,
RA Barnwell J.W.;
RT "Plasmodium vivax merozoite surface protein PvMSP-3beta is radically
RT polymorphic through mutation and large insertions and deletions.";
RL Infect. Genet. Evol. 4:309-319(2004).
DR EMBL; AY454095; AAS10481.1; -.
KW Merozoite.
FT NON TER 927 927
SQ SEQUENCE 927 AA; 99734 MW; B5DCBD6130A7F4E1 CRC64;

Query Match 64.3%; Score 45; DB 2; Length 927;
Best Local Similarity 78.6%; Pred. No. 89;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 EAAKYEAYKAAAAA 14
Db 722 EAAKEEAQKAATAA 735

RESULT 14
Q6DLT8 ID Q6DLT8 PRELIMINARY; PRT; 501 AA.
AC Q6DLT8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Voltage-dependent para-like sodium channel (Fragment).
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7160;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu J.-H., Zhao T.-Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY663380; AAT69676.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR005821; Ion.trans.
DR InterPro; IPR005820; M+channel_nlg.
```


DR Pfam; PF00520; Ion_trans; 2.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 501 501
SQ SEQUENCE 501 AA; 56497 MW; B66CD123B5EC5FDD CRC64;

Query Match 62.9%; Score 44; DB 2; Length 501;
Best Local Similarity 73.3%; Pred.No. 73;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAAKYEAYKAAAAA 15
Db 76 KAAKLEAQAAAAA 90

RESULT 15

Q6DLT7 PRELIMINARY; PRT; 509 AA.
AC Q6DLT7;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Voltage-dependent para-like sodium channel (Fragment).
OS Aedes albopictus (Forest day mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes.
OX NCBI_TaxID=7160;
RN [1]
RP SEQUENCE FROM N.A.
RA Wu J.-H., Zhao T.-Y.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY663381; AAT69677.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005261; F:cation channel activity; IEA.
DR GO; GO:0006812; P:cation transport; IEA.
DR InterPro; IPR005821; Ion trans.
DR InterPro; IPR005820; M+channel_nlg.
DR Pfam; PF00520; Ion_trans; 2.
KW Ion transport; Ionic channel; Transmembrane; Transport.
FT NON_TER 1
FT NON_TER 509 509
SQ SEQUENCE 509 AA; 56992 MW; 2D3DCB47D423D5C0 CRC64;

Query Match 62.9%; Score 44; DB 2; Length 509;
Best Local Similarity 73.3%; Pred.No. 74;
Matches 11; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 1 EAAKYEAYKAAAAA 15
Db 76 KAAKLEAQAAAAA 90

Search completed: March 31, 2005, 02:41:07
Job time : 82.5645 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 100.629 Seconds
(without alignments)
65.338 Million cell updates/sec

Title: US-10-056-583A-88
Perfect score: 82
Sequence: 1 APEKAKYEAYKAAAAA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	82	100.0	17	5	ABP52294	Abp52294 HLA-DR2 m
2	82	100.0	19	5	ABP52295	Abp52295 HLA-DR2 m
3	73	89.0	17	5	ABP52303	Abp52303 HLA-DR2 m
4	71	86.6	15	5	ABP52271	Abp52271 HLA-DR2 m
5	71	86.6	15	5	ABP52298	Abp52298 HLA-DR2 m
6	71	86.6	17	5	ABP52296	Abp52296 HLA-DR2 m
7	69	84.1	17	5	ABP52302	Abp52302 HLA-DR2 m
8	65	79.3	15	5	ABP52270	Abp52270 HLA-DR2 m
9	63	76.8	15	5	ABP52301	Abp52301 HLA-DR2 m
10	61	74.4	15	5	ABP52291	Abp52291 HLA-DR2 m
11	61	74.4	15	5	ABP52263	Abp52263 HLA-DR2 m
12	60	73.2	15	5	ABP52272	Abp52272 HLA-DR2 m
13	59	72.0	15	5	ABP52259	Abp52259 HLA-DR2 m
14	59	72.0	15	5	ABP52257	Abp52257 HLA-DR2 m
15	57	69.5	15	5	ABP52297	Abp52297 HLA-DR2 m
16	56	68.3	15	5	ABP52253	Abp52253 HLA-DR2 m
17	56	68.3	15	5	ABP52251	Abp52251 HLA-DR2 m
18	56	68.3	15	5	ABP52239	Abp52239 HLA-DR2 m
19	55	67.1	15	5	ABP52290	Abp52290 HLA-DR2 m
20	55	67.1	15	5	ABP52261	Abp52261 HLA-DR2 m
21	55	67.1	15	5	ABP52244	Abp52244 HLA-DR2 m
22	55	67.1	15	5	ABP52292	Abp52292 HLA-DR2 m
23	55	67.1	15	5	ABP52269	Abp52269 HLA-DR2 m
24	55	67.1	15	5	ABP52262	Abp52262 HLA-DR2 m
25	54	65.9	15	5	ABP52264	Abp52264 HLA-DR2 m

26	54	65.9	15	5	ABP52267	Abp52267 HLA-DR2 m
27	54	65.9	15	5	ABP52236	Abp52236 HLA-DR2 m
28	53	64.6	15	5	ABP52299	Abp52299 HLA-DR2 m
29	52	63.4	15	5	ABP52265	Abp52265 HLA-DR2 m
30	51	62.2	15	5	ABP52254	Abp52254 HLA-DR2 m
31	51	62.2	15	5	ABP52255	Abp52255 HLA-DR2 m
32	51	62.2	15	5	ABP52240	Abp52240 HLA-DR2 m
33	51	62.2	15	5	ABP52241	Abp52241 HLA-DR2 m
34	51	62.2	15	5	ABP52304	Abp52304 HLA-DR2 m
35	51	62.2	15	5	ABP52248	Abp52248 HLA-DR2 m
36	51	62.2	15	5	ABP52249	Abp52249 HLA-DR2 m
37	50	61.0	15	5	ABP52232	Abp52232 HLA-DR2 m
38	50	61.0	15	5	ABP52268	Abp52268 HLA-DR2 m
39	50	61.0	15	5	ABP52231	Abp52231 HLA-DR2 m
40	50	61.0	570	6	ADA55549	Ada55549 Human pro
41	50	61.0	570	7	ADJ70708	Adj70708 Human hea
42	49	59.8	15	5	ABP52235	Abp52235 HLA-DR2 m
43	49	59.8	15	5	ABP52250	Abp52250 HLA-DR2 m
44	48	58.5	15	5	ABP52277	Abp52277 HLA-DR2 m
45	48	58.5	15	5	ABP52238	Abp52238 HLA-DR2 m

ALIGNMENTS

RESULT 1
ABP52294
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX

OS Homo sapiens.
OS Synthetic.

XX WO200259143-A2.

PD 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

XX Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 100.0%; Score 82; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APEKAKYEAYKAAAAA 17
Db 1 APEKAKYEAYKAAAAA 17
RESULT 2
ABP52295
ID ABP52295 standard; peptide; 19 AA.
XX
AC ABP52295;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
XX demyelinating disease, e.g. multiple sclerosis, or post-viral
XX encephalomyelitis.
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX residues. The complex of the peptide with a major histocompatibility
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX immune response. (I) has antiinflammatory and neuroprotective activities,
XX and can be used as a MHC class II protein inhibitor. The compositions
XX comprising the peptides are useful for treating demyelinating diseases
XX such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
XX demyelinating condition, and a side effect of administering an anti-
XX tumour necrosis factor agents. The peptide further inhibits proliferation
XX of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
XX ABP52305 represent peptides used in the exemplification of the present
XX invention

SQ Sequence 19 AA;
Query Match 100.0%; Score 82; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 APEKAKYEAYKAAAAA 17
Db 1 APEKAKYEAYKAAAAA 17
RESULT 3
ABP52303
ID ABP52303 standard; peptide; 17 AA.
XX
AC ABP52303;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
XX
PD 01-AUG-2002.
XX
XX 24-JAN-2002; 2002WO-US002071.
XX
XX 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
XX demyelinating disease, e.g. multiple sclerosis, or post-viral
XX encephalomyelitis.
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide
XX with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
XX residues. The complex of the peptide with a major histocompatibility
XX complex (MHC) class II HLA-DR2 protein is involved in modulating an
XX immune response. (I) has antiinflammatory and neuroprotective activities,
XX and can be used as a MHC class II protein inhibitor. The compositions
XX comprising the peptides are useful for treating demyelinating diseases
XX such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
XX demyelinating condition, and a side effect of administering an anti-
XX tumour necrosis factor agents. The peptide further inhibits proliferation
XX of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
XX ABP52305 represent peptides used in the exemplification of the present
XX invention
SQ Sequence 17 AA;
Query Match 89.0%; Score 73; DB 5; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 APEKAKYEAYKAAAAA 17

```
Db      |||||:|||||
1 APERAKFEAYKAAAAA 17

RESULT 4
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match      86.6%; Score 71; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 EKAKYEAYKAAAAA 17
Db      |||||:|||||
1 EKAKYEAYKAAAAA 15

RESULT 6
ABP52296
ID ABP52296 standard; peptide; 17 AA.
XX
AC ABP52296;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
```

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 86.6%; Score 71; DB 5; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 EKAKYEAYKAAAAA 17
Db 1 EKAKYEAYKAAAAA 15
RESULT 7
ABP52302
ID ABP52302 standard; peptide; 17 AA.
XX
AC ABP52302;
XX
XX 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX

OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 84.1%; Score 69; DB 5; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00021;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 APEKAKYEAYKAAAAA 17
Db 1 APEKAKFEAFKAAAAA 17
RESULT 8
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
AC ABP52270;
XX
XX 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX

PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
PT
XX
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention
XX
SQ Sequence 15 AA;
Query Match 79.3%; Score 65; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0085;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 3 EKAKYEAYKAAAAA 17
Db 1 EAAKYEAYKAAAAA 15
RESULT 9
ABP52301
ID ABP52301 standard; peptide; 15 AA.
XX
AC ABP52301;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:95.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
PT
XX
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention
XX
SQ Sequence 15 AA;
Query Match 76.8%; Score 63; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0018;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 EKAKYEAYKAAAAA 17
Db 1 EKAKFEAFKAAAAA 15
RESULT 10
ABP52291
ID ABP52291 standard; peptide; 15 AA.
XX
AC ABP52291;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:85.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
XX (HARD) HARVARD COLLEGE.
PA
XX Strominger JL, Fridkis-Hareli M;
PI
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.
PT
XX
PS Claim 28; Page 39; 54pp; English.
XX
XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention
XX
SQ Sequence 15 AA;
Query Match 76.8%; Score 63; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0018;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 EKAKYEAYKAAAAA 17
Db 1 EKAKFEAFKAAAAA 15

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 74.4%; Score 61; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0039;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
Db 1 EKPKYEAYKAAAAA 15

RESULT 11

ABP52263

ID ABP52263 standard; peptide; 15 AA.

AC ABP52263;

XX 16-OCT-2002 (first entry)

XX HLA-DR2 molecule binding peptide SEQ ID NO:57.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

OS WO200259143-A2.

PN 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

XX Example 1; Page 33; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX SQ Sequence 15 AA;

Query Match 74.4%; Score 61; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0039;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
Db 1 EEAKYAAYKAAAAA 15

RESULT 12

ABP52272

ID ABP52272 standard; peptide; 15 AA.

XX AC ABP52272;

XX 16-OCT-2002 (first entry)

XX HLA-DR2 molecule binding peptide SEQ ID NO:66.

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC; HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis; immune response; antiinflammatory; neuroprotective; proliferation; MHC class II protein inhibitor; demyelinating disease; inhibition; post-viral encephalomyelitis; post-vaccine demyelinating condition; anti-tumour necrosis factor agent.

XX Homo sapiens.

OS Synthetic.

XX WO200259143-A2.

XX 01-AUG-2002.

XX 24-JAN-2002; 2002WO-US002071.

XX 24-JAN-2001; 2001US-0263569P.

XX (HARD) HARVARD COLLEGE.

PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 73.2%; Score 60; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0057;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
| | | | | | | | | | | | | | |
Db 1 EAKYEAYKAAAAA 15

RESULT 13
ABP52259
ID ABP52259 standard; peptide; 15 AA.
XX
AC ABP52259;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:53.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
CC New compositions comprising synthetic peptides in complex with a major
CC histocompatibility complex class II HLA-DR2 protein, useful for treating a
CC demyelinating disease, e.g. multiple sclerosis, or post-viral
CC encephalomyelitis.
XX
PS Example 1; Page 33; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 72.0%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0083;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
| | | | | | | | | | | | | | |
Db 1 EKAAYAAYKAAAAA 15

RESULT 14
ABP52257
ID ABP52257 standard; peptide; 15 AA.
XX
AC ABP52257;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
CC New compositions comprising synthetic peptides in complex with a major
CC histocompatibility complex class II HLA-DR2 protein, useful for treating a
CC demyelinating disease, e.g. multiple sclerosis, or post-viral
CC encephalomyelitis.
XX
PS Example 1; Page 32; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 72.0%; Score 59; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0083;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
| | | | | | | | | | | | | | |
Db 1 EAAKYAAYKAAAAA 15

RESULT 15
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX
AC ABP52297;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 69.5%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.018;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
|||:|||||||
Db 1 EKPKFEAYKAAAPA 15

Search completed: March 31, 2005, 02:35:27
Job time : 100.629 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:53 ; Search time 26.0484 Seconds
(without alignments)
48.718 Million cell updates/sec

Title: US-10-056-583A-88
Perfect score: 82
Sequence: 1 APEKAYEAYKAAAAA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	44	53.7	596	2	US-08-836-620A-16
2	43	52.4	162	4	US-09-732-210-1445
3	43	52.4	324	4	US-09-248-796A-17156
4	42	51.2	13	5	PCT-US95-04121-38
5	42	51.2	190	4	US-09-902-540-14713
6	42	51.2	273	4	US-09-910-430-34
7	42	51.2	1001	4	US-09-248-796A-18658
8	41	50.0	402	4	US-09-248-796A-17859
9	40	48.8	13	5	PCT-US94-10257A-33
10	40	48.8	56	4	US-09-405-743A-3
11	40	48.8	56	4	US-09-816-989A-3
12	40	48.8	77	4	US-09-405-743A-5
13	40	48.8	77	4	US-09-816-989A-5
14	40	48.8	86	4	US-09-405-743A-6
15	40	48.8	86	4	US-09-816-989A-6
16	40	48.8	109	4	US-09-405-743A-7
17	40	48.8	109	4	US-09-816-989A-7
18	40	48.8	466	4	US-09-489-039A-13950
19	40	48.8	802	4	US-09-489-039A-11230
20	40	48.8	1156	4	US-09-198-452A-171
21	40	48.8	1562	4	US-09-438-185A-152
22	39	47.6	38	3	US-09-117-121-16
23	39	47.6	38	3	US-09-117-121-24
24	39	47.6	38	4	US-09-344-529-5
25	39	47.6	166	4	US-09-252-991A-22139
26	39	47.6	202	4	US-09-205-258-344
27	39	47.6	219	4	US-09-902-540-16623

28	39	47.6	309	4	US-09-107-532A-6391	Sequence 6391, Ap
29	39	47.6	411	4	US-09-248-796A-18456	Sequence 18456, A
30	39	47.6	497	1	US-08-295-670-6	Sequence 6, Appli
31	39	47.6	497	1	US-08-633-485-6	Sequence 6, Appli
32	39	47.6	510	3	US-08-508-761B-4	Sequence 4, Appli
33	39	47.6	601	4	US-09-252-991A-21824	Sequence 21824, A
34	39	47.6	731	4	US-09-252-991A-18769	Sequence 18769, A
35	38.5	47.0	459	4	US-09-543-681A-5116	Sequence 5116, Ap
36	38	46.3	54	3	US-09-117-121-30	Sequence 30, Appl
37	38	46.3	163	2	US-08-245-511-2	Sequence 2, Appli
38	38	46.3	163	2	US-08-600-993A-2	Sequence 2, Appli
39	38	46.3	171	4	US-10-144-198-28	Sequence 28, Appl
40	38	46.3	186	4	US-09-902-540-11242	Sequence 11242, A
41	38	46.3	319	4	US-09-270-767-45793	Sequence 45793, A
42	38	46.3	333	4	US-09-198-452A-652	Sequence 652, App
43	38	46.3	335	4	US-09-438-185A-615	Sequence 615, App
44	38	46.3	351	4	US-09-489-039A-7442	Sequence 7442, Ap
45	38	46.3	391	4	US-09-328-352-4861	Sequence 4861, Ap

ALIGNMENTS

RESULT 1
US-08-836-620A-16
; Sequence 16, Application US/08836620A
; Patent No. 5958710
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Orphan receptor
; NUMBER OF SEQUENCES: 19
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,620A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03933
; FILING DATE:
; APPLICATION NUMBER: GB 9518272.1
; FILING DATE: 08-SEP-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9605550.4
; FILING DATE: 15-MAR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9607532.0
; FILING DATE: 11-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9609576.5
; FILING DATE: 08-MAY-1996
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 596 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; ORGANISM: Rattus rattus
US-08-836-620A-16

Query Match 53.7%; Score 44; DB 2; Length 596;
Best Local Similarity 68.8%; Pred. No. 28;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 2 PEKAKYEAYKAAAAA 17
Db 55 PEGAAAYEFNAAAAAA 70

RESULT 2
US-09-732-210-1445

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; Sequence 1445, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.
; APPLICANT: Liang, Jihong
; APPLICANT: Mittanck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 1445
; LENGTH: 162
; TYPE: PRT
; ORGANISM: Mycobacterium tuberculosis
US-09-732-210-1445

Query Match          52.4%; Score 43; DB 4; Length 162;
Best Local Similarity 52.9%; Pred. No. 9.9;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAAAA 17
Db      97 APKPSKLEVENAALAA 113

RESULT 3
US-09-248-796A-17156
; Sequence 17156, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 17156
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-17156

Query Match          52.4%; Score 43; DB 4; Length 324;
Best Local Similarity 71.4%; Pred. No. 21;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAA 14
Db      157 APEKAKEESAPAAA 170

RESULT 4
PCT-US95-04121-38
; Sequence 38, Application PC/TUS9504121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
; NUMBER OF SEQUENCES: 62
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04121
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222,206
; FILING DATE: April 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 079.2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04121-38

Query Match          51.2%; Score 42; DB 5; Length 13;
Best Local Similarity 76.9%; Pred. No. 0.93;
Matches 10; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      5 AKYEAYKAAAAAA 17
Db      1 AAYKAAKAAAAAA 13

RESULT 5
US-09-902-540-14713
; Sequence 14713, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14713
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-14713

Query Match          51.2%; Score 42; DB 4; Length 190;
Best Local Similarity 50.0%; Pred. No. 17;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAA 14
Db      120 APERTEYRVWRAAA 133

RESULT 6
US-09-910-430-34
; Sequence 34, Application US/09910430
; Patent No. 6794166
; GENERAL INFORMATION:
; APPLICANT: Godfroi, Edmond
; APPLICANT: Bollen, Alex

```

; APPLICANT: Lebouille, Gerard
; TITLE OF INVENTION: IDENTIFICATION AND MOLECULAR CHARACTERIZATION OF
; TITLE OF INVENTION: PROTEINS, EXPRESSED IN THE IXODES RICINUS SALIVARY
; TITLE OF INVENTION: GLANDS

; FILE REFERENCE: VANM229.001CP1
; CURRENT APPLICATION NUMBER: US/09/910,430
; CURRENT FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: PCT/BE00/00061
; PRIOR FILING DATE: 2000-06-06
; PRIOR APPLICATION NUMBER: GB 9913425.6
; PRIOR FILING DATE: 1999-06-09

; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34

; LENGTH: 273
; TYPE: PRT

; ORGANISM: Ixodes ricinus

US-09-910-430-34

Query Match 51.2%; Score 42; DB 4; Length 273;
Best Local Similarity 52.9%; Pred. No. 26;
Matches 9; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17

Db 203 APAVASYQTYHAAPAVA 219

RESULT 7

US-09-248-796A-18658
; Sequence 18658, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 18658

; LENGTH: 1001

; TYPE: PRT

; ORGANISM: Candida albicans

; FEATURE:

; NAME/KEY: UNSURE

; LOCATION: (21)

; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno

US-09-248-796A-18658

Query Match 51.2%; Score 42; DB 4; Length 1001;

Best Local Similarity 78.6%; Pred. No. 1.1e+02;

Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 KAKYEAYKAAAAA 17

Db 818 KAKEEAEAAAAA 831

RESULT 8

US-09-248-796A-17859
; Sequence 17859, Application US/09248796A
; Patent No. 6747137

; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132

; CURRENT APPLICATION NUMBER: US/09/248,796A

Query Match 48.8%; Score 40; DB 5; Length 13;

Best Local Similarity 76.9%; Pred. No. 2;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AKYEAYKAAAAA 17

; CURRENT FILING DATE: 1999-02-12

; PRIOR APPLICATION NUMBER: US 60/074,725

; PRIOR FILING DATE: 1998-02-13

; PRIOR APPLICATION NUMBER: US 60/096,409

; PRIOR FILING DATE: 1998-08-13

; NUMBER OF SEQ ID NOS: 28208

; SEQ ID NO 17859

; LENGTH: 402

; TYPE: PRT

; ORGANISM: Candida albicans

US-09-248-796A-17859

Query Match 50.0%; Score 41; DB 4; Length 402;

Best Local Similarity 80.0%; Pred. No. 57;

Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 KAKYEAYKAA 13

Db 70 KAKYESYDAA 79

RESULT 9

PCT-US94-10257A-33

; Sequence 33, Application PC/TUS9410257A

; GENERAL INFORMATION:
; APPLICANT: IMMULOGIC PHARMACEUTICAL CORPORATION

; APPLICANT: BRIGITTE DEVAUX

; APPLICANT: JONATHAN B. ROTHBARD

; APPLICANT: DAWN SMILEK

; TITLE OF INVENTION: USES OF MYELIN OLIGODENDROCYTE

; TITLE OF INVENTION: GLYCOPROTEIN AND PEPTIDE PORTIONS THEREOF IN PROTOCOLS

; TITLE OF INVENTION: RELATED TO AUTOIMMUNE DISEASE

; NUMBER OF SEQUENCES: 95

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION

; STREET: 610 LINCOLN STREET

; CITY: WALTHAM

; STATE: Massachusetts

; COUNTRY: USA

; ZIP: 02145

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: ASCII text

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10257A

; FILING DATE: 1 SEPTEMBER 1994

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/116,824

; FILING DATE: 03-SEP-1993

; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: ANNE I CRAIG

; REGISTRATION NUMBER: 32,976

; REFERENCE/DOCKET NUMBER: 071.1 PCT

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000

; TELEFAX: (617) 466-6040

; INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

PCT-US94-10257A-33

Query Match 48.8%; Score 40; DB 5; Length 13;

Best Local Similarity 76.9%; Pred. No. 2;

Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 AKYEAYKAAAAA 17

Db 1 AAYAAAKKAAAAA 13
| | | | | | | |

RESULT 10

US-09-405-743A-3
; Sequence 3, Application US/09405743A
; Patent No. 6514938

GENERAL INFORMATION:

; APPLICANT: Yeda Research and Development Co., Ltd.

; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

; FILE REFERENCE: 60807-A

; CURRENT APPLICATION NUMBER: US/09/405,743A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3

; LENGTH: 56

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

; OTHER INFORMATION: PEPTIDE

US-09-405-743A-3

Query Match 48.8%; Score 40; DB 4; Length 56;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAA 15
| : | : | : | : |

Db 18 AAKKAEAKAYKAAEA 32

RESULT 11

US-09-816-989A-3

; Sequence 3, Application US/09816989A
; Patent No. 6800287

GENERAL INFORMATION:

; APPLICANT: Gad, Alexander

; APPLICANT: Lis, Doris

; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS

; TITLE OF INVENTION: AND FOR THERAPEUTIC USE

; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816,989A

; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/101,693

; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: PCT/US99/22402

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 3

; LENGTH: 56

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

US-09-816-989A-3

Query Match 48.8%; Score 40; DB 4; Length 56;
Best Local Similarity 60.0%; Pred. No. 9.7;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAA 15
| : | : | : | : |

Db 18 AAKKAEAKAYKAAEA 32

RESULT 12

US-09-405-743A-5

; Sequence 5, Application US/09405743A
; Patent No. 6514938

; GENERAL INFORMATION:
; APPLICANT: Yeda Research and Development Co., Ltd.
; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS
; FILE REFERENCE: 60807-A

; CURRENT APPLICATION NUMBER: US/09/405,743A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 5

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC

; OTHER INFORMATION: PEPTIDE

US-09-405-743A-5

Query Match 48.8%; Score 40; DB 4; Length 77;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAA 15
| : | : | : | : |

Db 18 AAKKAEAKAYKAAEA 32

RESULT 13

US-09-816-989A-5

; Sequence 5, Application US/09816989A
; Patent No. 6800287

GENERAL INFORMATION:

; APPLICANT: Gad, Alexander

; APPLICANT: Lis, Doris

; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARKERS

; TITLE OF INVENTION: AND FOR THERAPEUTIC USE

; FILE REFERENCE: 2609/60807-A-PCT-US

; CURRENT APPLICATION NUMBER: US/09/816,989A

; CURRENT FILING DATE: 2001-03-23

; PRIOR APPLICATION NUMBER: 60/101,693

; PRIOR FILING DATE: 1998-09-25

; PRIOR APPLICATION NUMBER: PCT/US99/22402

; PRIOR FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 5

; LENGTH: 77

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide

US-09-816-989A-5

Query Match 48.8%; Score 40; DB 4; Length 77;
Best Local Similarity 60.0%; Pred. No. 14;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAA 15
| : | : | : | : |

Db 18 AAKKAEAKAYKAAEA 32

RESULT 14

US-09-405-743A-6

; Sequence 6, Application US/09405743A
; Patent No. 6514938

GENERAL INFORMATION:

; APPLICANT: Yeda Research and Development Co., Ltd.

; TITLE OF INVENTION: GLATIRAMER ACETATE MOLECULAR WEIGHT MARKERS

; FILE REFERENCE: 60807-A

; CURRENT APPLICATION NUMBER: US/09/405,743A

; CURRENT FILING DATE: 1999-09-24

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: SYNTHETIC
; OTHER INFORMATION: PEPTIDE
US-09-405-743A-6

Query Match 48.8%; Score 40; DB 4; Length 86;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAA 15
| :||: :||| |
Db 18 AAKKAEAKAYKAAEA 32

RESULT 15
US-09-816-989A-6
; Sequence 6, Application US/09816989A
; Patent No. 6800287
; GENERAL INFORMATION:
; APPLICANT: Gad, Alexander
; APPLICANT: Lis, Doris
; TITLE OF INVENTION: COPOLYMER 1 RELATED POLYPEPTIDES FOR USE AS MOLECULAR WEIGHT MARK
; TITLE OF INVENTION: AND FOR THERAPEUTIC USE
; FILE REFERENCE: 2609/60807-A-PCT-US
; CURRENT APPLICATION NUMBER: US/09/816,989A
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/101,693
; PRIOR FILING DATE: 1998-09-25
; PRIOR APPLICATION NUMBER: PCT/US99/22402
; PRIOR FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic Peptide
US-09-816-989A-6

Query Match 48.8%; Score 40; DB 4; Length 86;
Best Local Similarity 60.0%; Pred. No. 16;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAA 15
| :||: :||| |
Db 18 AAKKAEAKAYKAAEA 32

Search completed: March 31, 2005, 02:44:08
Job time : 27.0484 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 75.4032 Seconds
(without alignments)
74.648 Million cell updates/sec

Title: US-10-056-583A-88
Perfect score: 82
Sequence: 1 APEKAKYEAYKAAAAA 17

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Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
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- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	82	100.0	17	14	US-10-056-583-88	Sequence 88, Appl
2	82	100.0	19	14	US-10-056-583-89	Sequence 89, Appl
3	73	89.0	17	14	US-10-056-583-97	Sequence 97, Appl
4	71	86.6	15	14	US-10-056-583-65	Sequence 65, Appl
5	71	86.6	17	14	US-10-056-583-90	Sequence 90, Appl
6	69	84.1	17	14	US-10-056-583-96	Sequence 96, Appl
7	65	79.3	15	14	US-10-056-583-64	Sequence 64, Appl
8	63	76.8	15	14	US-10-056-583-95	Sequence 95, Appl
9	62	75.6	15	14	US-10-056-583-92	Sequence 92, Appl
10	61	74.4	15	14	US-10-056-583-57	Sequence 57, Appl
11	61	74.4	15	14	US-10-056-583-85	Sequence 85, Appl
12	60	73.2	15	14	US-10-056-583-66	Sequence 66, Appl
13	59	72.0	15	14	US-10-056-583-51	Sequence 51, Appl

14	59	72.0	15	14	US-10-056-583-53	Sequence 53, Appl
15	57	69.5	15	14	US-10-056-583-91	Sequence 91, Appl
16	56	68.3	15	14	US-10-056-583-33	Sequence 33, Appl
17	56	68.3	15	14	US-10-056-583-45	Sequence 45, Appl
18	56	68.3	15	14	US-10-056-583-47	Sequence 47, Appl
19	55	67.1	15	14	US-10-056-583-38	Sequence 38, Appl
20	55	67.1	15	14	US-10-056-583-55	Sequence 55, Appl
21	55	67.1	15	14	US-10-056-583-56	Sequence 56, Appl
22	55	67.1	15	14	US-10-056-583-63	Sequence 63, Appl
23	55	67.1	15	14	US-10-056-583-84	Sequence 84, Appl
24	55	67.1	15	14	US-10-056-583-86	Sequence 86, Appl
25	54	65.9	15	14	US-10-056-583-30	Sequence 30, Appl
26	54	65.9	15	14	US-10-056-583-58	Sequence 58, Appl
27	54	65.9	15	14	US-10-056-583-61	Sequence 61, Appl
28	53	64.6	15	14	US-10-056-583-93	Sequence 93, Appl
29	52	63.4	15	14	US-10-056-583-59	Sequence 59, Appl
30	51	62.2	15	14	US-10-056-583-34	Sequence 34, Appl
31	51	62.2	15	14	US-10-056-583-35	Sequence 35, Appl
32	51	62.2	15	14	US-10-056-583-42	Sequence 42, Appl
33	51	62.2	15	14	US-10-056-583-43	Sequence 43, Appl
34	51	62.2	15	14	US-10-056-583-48	Sequence 48, Appl
35	51	62.2	15	14	US-10-056-583-49	Sequence 49, Appl
36	51	62.2	15	14	US-10-056-583-98	Sequence 98, Appl
37	50	61.0	15	14	US-10-056-583-25	Sequence 25, Appl
38	50	61.0	15	14	US-10-056-583-26	Sequence 26, Appl
39	50	61.0	15	14	US-10-056-583-62	Sequence 62, Appl
40	50	61.0	570	15	US-10-094-749-3117	Sequence 3117, Ap
41	50	61.0	570	16	US-10-408-765A-2514	Sequence 2514, Ap
42	49	59.8	15	14	US-10-056-583-29	Sequence 29, Appl
43	49	59.8	15	14	US-10-056-583-44	Sequence 44, Appl
44	48	58.5	15	14	US-10-056-583-32	Sequence 32, Appl
45	48	58.5	15	14	US-10-056-583-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

Query Match 100.0%; Score 82; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.6e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
| | | | | | | | | | | | | | | | |
Db 1 APEKAKYEAYKAAAAA 17

RESULT 2
US-10-056-583-89

```
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89
```

```
Query Match          100.0%; Score 82; DB 14; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 APEKAKVEAYKAAAAA 17
         |||||
Db       1 APEKAKVEAYKAAAAA 17
```

```
RESULT 3
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match          89.0%; Score 73; DB 14; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.7e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 APEKAKVEAYKAAAAA 17
         |||||
Db       1 APEKAKFEAYKAAAP 17
```

```
RESULT 4
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match          86.6%; Score 71; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.6e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 EKAKYEAYKAAAAA 17
         |||||
Db       1 EKAKYEAYKAAAAA 15
```

```
RESULT 5
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match          86.6%; Score 71; DB 14; Length 17;
Best Local Similarity 100.0%; Pred. No. 9.8e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 EKAKYEAYKAAAAA 17
         |||||
Db       1 EKAKYEAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
```

```
Query Match      84.1%; Score 69; DB 14; Length 17;
Best Local Similarity 82.4%; Pred. No. 0.00021;
Matches 14; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 APEKAKYEAYKAAAAAA 17
        |||||:|||||
Db      1 APEKAKFEAFKAAAAAPA 17
```

```
RESULT 7
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64
```

```
Query Match      79.3%; Score 65; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00081;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 EKAKYEAYKAAAAAA 17
        |||||:|||||
Db      1 EAAKYEAYKAAAAAA 15
```

```
RESULT 8
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
```

```
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95
```

```
Query Match      76.8%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0017;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      3 EKAKYEAYKAAAAAA 17
        |||||:|||||
Db      1 EKAKFEAFKAAAAAA 15
```

```
RESULT 9
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92
```

```
Query Match      75.6%; Score 62; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0025;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      3 EKAKYEAYKAAAAAA 17
        |||||:|||||
Db      1 EKAKYEAYKAAAAAA 15
```

```
RESULT 10
US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57

Query Match 74.4%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0036;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
|:|||||
Db 1 EAKYAAYKAAAAA 15

RESULT 11

US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Strominger and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

Query Match 74.4%; Score 61; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0036;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
|||:|||||
Db 1 EKPKYEAYKAAAPA 15

RESULT 12

US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Strominger and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

Query Match 73.2%; Score 60; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0052;

Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
|:|||||
Db 1 EAKYEAYKAAAAA 15

RESULT 13
US-10-056-583-51
; Sequence 51, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51

Query Match 72.0%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0076;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
|:|||||
Db 1 EAKYAAYKAAAAA 15

RESULT 14
US-10-056-583-53
; Sequence 53, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-53

Query Match 72.0%; Score 59; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0076;
Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 17
|||:|||||
Db 1 EAKYAAYKAAAAA 15

RESULT 15
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

Query Match 69.5%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.016;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 EKAKYEAYKAAAAA 17
||:|||||||
Db 1 EKPKEAYKAAAAA 15

Search completed: March 31, 2005, 02:48:48
Job time : 75.4032 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 20.2903 Seconds
(without alignments)
80.614 Million cell updates/sec

Title: US-10-056-583A-88
Perfect score: 82
Sequence: 1 APEKAKYEAYKAAAAA 17
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5 .

Searched: 283416 seqs, 96216763 residues 283416
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	45	54.9	154	2	H81076	conserved hypothet
2	45	54.9	154	2	B81866	conserved hypothet
3	45	54.9	179	2	F97683	50S ribosomal prot
4	45	54.9	179	2	AF2908	50S ribosomal prot
5	44.5	54.3	189	2	S77930	exoskeletal protei
6	44.5	54.3	189	2	S77935	exoskeletal protei
7	44	53.7	599	1	QRMSE	estrogen receptor
8	44	53.7	600	1	QRRTE	estrogen receptor
9	43	52.4	162	2	H70927	probable rpsp prot
10	43	52.4	185	2	S36290	T-cell receptor ga
11	43	52.4	347	2	A81794	probable rotamase
12	43	52.4	348	2	B81216	peptidyl-prolyl ci
13	43	52.4	421	2	JV0057	tola protein - Esc
14	43	52.4	441	2	A43555	GAP-43-related pro
15	42	51.2	188	2	I50145	homeotic protein H
16	42	51.2	289	2	A43562	homeotic protein H
17	42	51.2	329	2	D96030	hypothetical prote
18	42	51.2	1167	2	D97516	DNA polymerase III
19	42	51.2	1167	2	AD2735	DNA polymerase III
20	41	50.0	88	2	JC2184	transcription fact
21	41	50.0	129	1	TNLJG3	trans-activating t
22	41	50.0	177	2	AD1307	peptidyl methionin
23	41	50.0	177	2	AD1679	peptidyl methionin
24	41	50.0	254	2	H86355	probable 14-3-3 pr
25	41	50.0	289	2	AC1399	hypothetical prote
26	41	50.0	641	2	PH1919	FL-160-4 protein -
27	41	50.0	1885	1	JC4086	fatty-acid synthas
28	41	50.0	2129	2	T27431	hypothetical prote
29	40	48.8	73	2	S40015	phd protein - phg

30	40	48.8	75	2	S61806	M-like protein enn
31	40	48.8	106	1	TNLJS2	trans-activating t
32	40	48.8	107	2	AB3271	hypothetical prote
33	40	48.8	202	2	A83492	probable transcrip
34	40	48.8	377	2	T43037	probable fatty-aci
35	40	48.8	467	2	AC2015	hypothetical prote
36	40	48.8	478	2	S04675	H+-transporting tw
37	40	48.8	480	2	G70302	conserved hypothet
38	40	48.8	594	2	T50013	hypothetical prote
39	40	48.8	806	2	T13690	hypothetical prote
40	40	48.8	829	2	B64114	translation initia
41	40	48.8	1537	2	F86509	CT147 hypothetical
42	40	48.8	1537	2	C81558	conserved hypothet
43	40	48.8	1537	2	H72112	ct147 hypothetical
44	40	48.8	1842	2	T43409	probable fatty-aci
45	40	48.8	1842	2	T38781	fatty acid synthas

ALIGNMENTS

RESULT 1

H81076
conserved hypothetical protein NMB1500 [imported] - Neisseria meningitidis (strain MC58)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: H81076
R;Tetrelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81076
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <TET>
A;Cross-references: UNIPROT:Q9JYN4; GB:AE002499; GB:AE002098; NID:g7226737; PIDN:AAF4185
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1500
C;Superfamily: Escherichia coli ybdQ protein

Query Match 54.9%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. NO. 5.4;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAA 16
||| :|:|:|
Db 48 APEFLQHSYEAAVA 63

RESULT 2

B81866
conserved hypothetical protein NMA1703 [imported] - Neisseria meningitidis (strain Z2491)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: B81866
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: B81866
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-154 <PAR>
A;Cross-references: UNIPROT:Q9JTN1; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB8493
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA1703
C;Superfamily: Escherichia coli ybdQ protein

Query Match 54.9%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 5.4;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 16
||||:|:|:|
Db 48 APEFLQHESEYEAAVA 63

RESULT 3
F97683
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97683
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:g15157917; GSPDB:C
C;Genetics:
A;Gene: AGR_C_4900
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match 54.9%; Score 45; DB 2; Length 179;
Best Local Similarity 64.7%; Pred. No. 6.3;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
||||:|:|:|
Db 135 AEEKARLEAEKVAAQA 151

RESULT 4
AF2908
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2908
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan, Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:g17741210; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rplS
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match 54.9%; Score 45; DB 2; Length 179;
Best Local Similarity 64.7%; Pred. No. 6.3;
Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
||||:|:|:|
Db 135 AEEKARLEAEKVAAQA 151

RESULT 5
S77930
exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homarus americanus
A;Reference number: S77925
A;Accession: S77930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M496

Query Match 54.3%; Score 44.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 8;
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 APEKAK-YEAYKAAAAA 17
||||:|:|:|
Db 9 AAEKARFFQAFKAAEAAA 26

RESULT 6
S77935
exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77935
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homarus americanus
A;Reference number: S77925
A;Accession: S77935
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M495

Query Match 54.3%; Score 44.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 8;
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 APEKAK-YEAYKAAAAA 17
||||:|:|:|
Db 9 AAEKARFFQAFKAAEAAA 26

RESULT 7
QRMSE
estrogen receptor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Mar-1992 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: A40061
R;White, R.; Lees, J.A.; Needham, M.; Ham, J.; Parker, M.
Mol. Endocrinol. 1, 735-744, 1987
A;Title: Structural organization and expression of the mouse estrogen receptor.
A;Reference number: A40061; MUID:91042558; PMID:2484714
A;Accession: A40061
A;Molecule type: mRNA
A;Residues: 1-599 <WHI>
A;Cross-references: UNIPROT:P19785; GB:M38651; NID:g193179; PIDN:AAA37580.1; PID:g193180
C;Comment: The steroid hormones and their receptors are involved in the regulation of eukaryotic gene expression.
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly associated with DNA.
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone receptor
F;1-183/Domain: amino-terminal <NH2>
F;184-275/Domain: DNA binding #status predicted <DNA>
F;187-460/Domain: erba transforming protein homology <ERBA>

F;187-210/Region: zinc finger CCCC motif
F;223-245/Region: zinc finger CCCC motif
F;260-275/Region: nuclear location signal
F;304-556/Domain: steroid binding #status predicted <STB>
F;189,192,206,209/Binding site: zinc (Cys) #status predicted
F;225,231,241,244/Binding site: zinc (Cys) #status predicted
F;224,309/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.7%; Score 44; DB 1; Length 599;
Best Local Similarity 68.8%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAAA 17
||| ||| |||||
Db 55 PEGAAAYEFNAAAAA 70

RESULT 8
QRRTE
estrogen receptor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1991 #sequence_revision 14-Jul-1994 #text_change 09-Jul-2004
C;Accession: S07379; S16731
R;Koike, S.; Sakai, M.; Muramatsu, M.
Nucleic Acids Res. 15, 2499-2513, 1987.
A;Title: Molecular cloning and characterization of rat estrogen receptor cDNA.
A;Reference number: S07379; MUID:87174780; PMID:3031601
A;Accession: S07379
A;Molecule type: mRNA
A;Residues: 1-600 <KOI>
A;Cross-references: UNIPROT:P06211; EMBL:X00102; NID:g56110; PIDN:CAA68287.1; PID:g56111
R;Maggi, A.M.A.
submitted to the EMBL Data Library, June 1991
A;Reference number: S16731
A;Accession: S16731
A;Molecule type: mRNA
A;Residues: 1-487,'T',489-600 <MAG>
A;Cross-references: EMBL:X61098; NID:g56120; PIDN:CAA43411.1; PID:g56121
C;Comment: The steroid hormones and their receptors are involved in the regulation of eu
C;Comment: In the absence of ligand, steroid hormone receptors are thought to be weakly
complex appears to recognize discrete DNA sequences upstream of transcriptional start sit
C;Superfamily: estrogen receptor; erba transforming protein homology
C;Keywords: DNA binding; nucleus; phosphoprotein; steroid binding; steroid hormone recep
F;1-184/Domain: amino-terminal <NH2>
F;185-276/Domain: DNA binding #status predicted <DNA>
F;188-461/Domain: erba transforming protein homology <ERBA>
F;188-211/Region: zinc finger CCCC motif
F;224-246/Region: zinc finger CCCC motif
F;261-276/Region: nuclear location signal
F;305-557/Domain: steroid binding #status predicted <STB>
F;190,193,207,210/Binding site: zinc (Cys) #status predicted
F;226,232,242,245/Binding site: zinc (Cys) #status predicted
F;241,310/Binding site: phosphate (Ser) (covalent) #status predicted

Query Match 53.7%; Score 44; DB 1; Length 600;
Best Local Similarity 68.8%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAAA 17
||| ||| |||||
Db 55 PEGAAAYEFNAAAAA 70

RESULT 9
H70927
probable rpsP protein - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004
C;Accession: H70927
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998

A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: H70927
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-162 <COL>
A;Cross-references: UNIPROT:Q10795; GB:Z74024; GB:AL123456; NID:g3250700; PIDN:CAA98346.
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: rpsP

Query Match 52.4%; Score 43; DB 2; Length 162;
Best Local Similarity 52.9%; Pred. No. 12;
Matches 9; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
||: ||: ||: |||
Db 97 APKPSKLEVFNAALAA 113

RESULT 10
S36290
T-cell receptor gamma chain precursor - sheep (fragment)
C;Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36290; S23041
R;Hein, W.R.; Dudler, L.
EMBO J. 12, 715-724, 1993
A;Title: Divergent evolution of T cell repertoires: extensive diversity and developmenta
A;Reference number: S36287; MUID:93178447; PMID:8440261
A;Accession: S36290
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-185 <HEI>
A;Cross-references: EMBL:Z12998; NID:g2260; PIDN:CAA78342.1; PID:g2261
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: T-cell receptor

Query Match 52.4%; Score 43; DB 2; Length 185;
Best Local Similarity 66.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAA 14
: |||| |||
Db 81 DKAKYSVYKGAA 92

RESULT 11
A81794
probable rotamase NMA2206 [imported] - Neisseria meningitidis (strain Z2491 serogroup A)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: A81794
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: A81794
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-347 <PAR>
A;Cross-references: UNIPROT:Q9JSP0; GB:AL162758; GB:AL157959; NID:g7380672; PIDN:CAB8541
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMA2206

Query Match 52.4%; Score 43; DB 2; Length 347;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 10; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 16

Db 15 APOKAKTASAKAAKAA 30
||:|||| : |||| ||
RESULT 12
B81216
peptidyl-prolyl, cis-trans isomerase NMB0281 [imported] - Neisseria meningitidis (strain
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81216
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81216
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-348 <TET>
A;Cross-references: UNIPROT:Q9KI86; GB:AE002385; GB:AE002098; NID:g7225506; PIDN:AAF4073
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0281
Query Match 52.4%; Score 43; DB 2; Length 348;
Best Local Similarity 62.5%; Pred. No. 25;
Matches 10; Conservative 2; Mismatches 4; Indels 4; Gaps 0;
Qy 1 APEKAKYEAYKAAAA 16
||:|||| : |||| ||
Db 22 APOKAKTASAKAAKAA 37
RESULT 13
JV0057
tola protein - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: JV0057; B64810
R;Levengood, S.K.; Webster, R.E.
J. Bacteriol. 171, 6600-6609, 1989
A;Title: Nucleotide sequences of the tola and tolB genes and localization of their produ
A;Reference number: JV0057; MUID:90078104; PMID:2687247
A;Accession: JV0057
A;Molecule type: DNA
A;Residues: 1-421 <LEV>
A;Cross-references: UNIPROT:P19934; GB:M28232; NID:g148018; PIDN:AAA24683.1; PID:g148019
A;Experimental source: strain JM105
A;Note: the authors translated the initiation codon GTG for residue 1 as Val
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: B64810
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-421 <BLAT>
A;Cross-references: GB:AE000177; GB:U00096; NID:g1786955; PIDN:AAC73833.1; PID:g1786960;
A;Experimental source: strain K-12, substrain MGL555
C;Comment: tola and tolB proteins are necessary for colicins E2, E3, A, and K to reach t
C;Genetics:
A;Gene: tola
A;Map position: 17 min
A;Start codon: GTG
C;Keywords: nucleotide binding; P-loop; transmembrane protein
F;14-34/Domain: transmembrane #status predicted <MSS>
F;78-301/Domain: helical #status predicted <HSR>
F;355-362/Region: nucleotide-binding motif A (P-loop)
Query Match 52.4%; Score 43; DB 2; Length 421;

Best Local Similarity 73.3%; Pred. No. 30;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 1 APEKAKYEAYKAAAA 15
| |||| | ||||
Db 215 AAEKAKAEAEKAA 229
RESULT 14
A43555
GAP-43-related protein - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C;Accession: A43555; S65398
R;Ng, S.C.; Perkins, L.A.; Conboy, G.; Perrimon, N.; Fishman, M.C.
Development 105, 629-638, 1989
A;Title: A Drosophila gene expressed in the embryonic CNS shares one conserved domain wit
A;Reference number: A43555; MUID:90126372; PMID:2693037
A;Accession: A43555
A;Molecule type: mRNA
A;Residues: 1-441 <NGA>
A;Cross-references: UNIPROT:P29746; EMBL:X63828
R;Perkins, L.A.
submitted to the EMBL Data Library, December 1991
A;Reference number: S65398
A;Accession: S65398
A;Molecule type: mRNA
A;Residues: 1-111, 'AIPEKCTL', 120, 'EEAK', 125, 'AQENA', 131, 'VEAEKKQEKTAET', 146, 'EPTVEAQP',
A;Cross-references: EMBL:X63828; NID:g7663; PID:g7664
A;Note: the differences in residues 112-178 are due to frameshift errors
C;Genetics:
A;Gene: FlyBase:bnb
A;Cross-references: FlyBase:FBgn0001090
A;Map position: 10
Query Match 52.4%; Score 43; DB 2; Length 441;
Best Local Similarity 58.8%; Pred. No. 32;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
Qy 1 APEKAKYEAYKAAAA 17
| |||| | : |||||
Db 263 APEKKSIESSPAAAAAS 279
RESULT 15
I50145
homeotic protein Hox M - chicken
N;Alternate names: CHOX M
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 16-Aug-2004
C;Accession: I50145; S14512
R;Crompton, M.R.; MacGregor, A.D.; Goodwin, G.H.
Leukemia 5, 357-360, 1991
A;Title: cDNA cloning of a homeobox-containing gene expressed in avian myeloblastic viru
A;Reference number: I50145; MUID:91238215; PMID:1674560
A;Accession: I50145
A;Status: preliminary; translated from GB/EMBL/DBBJ
A;Molecule type: mRNA
A;Residues: 1-188 <CRO>
A;Cross-references: UNIPROT:P23459; EMBL:X57158; NID:g62700; PIDN:CAA40445.1; PID:g62701
C;Genetics:
A;Gene: CHOX M
C;Superfamily: homeobox homology
C;Keywords: DNA binding; homeobox; nucleus; transcription regulation
F;96-152/Domain: homeobox homology <HOX>
Query Match 51.2%; Score 42; DB 2; Length 188;
Best Local Similarity 81.8%; Pred. No. 20;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 7 YEAYKAAAAAA 17
| ||||| |||||
Db 10 YSKYKAAAAAA 20

Search completed: March 31, 2005, 02:42:28
Job time : 21.2903 secs

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OM protein - protein search, using sw model.

Run on: March 31, 2005, 02:18:02 ; Search time 91.3065 Seconds
(without alignments)
95.342 Million cell updates/sec

Title: US-10-056-583A-88
Perfect score: 82
Sequence: 1 APEKAKYEYKAAAAA 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	50	61.0	570	2 Q96M46	Q96m46 homo sapien
2	48	58.5	707	2 Q64CP3	Q64cp3 uncultured
3	45	54.9	154	2 Q9JTN1	Q9jtn1 neisseria m
4	45	54.9	154	2 Q9JYN4	Q9jyn4 neisseria m
5	45	54.9	179	1 RL19 AGRT5	Q8ubz5 agrobacteri
6	45	54.9	300	2 Q9VFL4	Q9vfl4 drosophila
7	45	54.9	375	2 Q75GC3	Q75gc3 oryza sativ
8	45	54.9	395	2 Q6D7F3	Q6d7f3 erwinia car
9	45	54.9	463	2 Q9V7U6	Q9v7u6 drosophila
10	44.5	54.3	189	2 Q7M495	Q7m495 homarus ame
11	44.5	54.3	189	2 Q7M496	Q7m496 homarus ame
12	44	53.7	113	2 Q6LAN9	Q6lan9 rattus norv
13	44	53.7	272	2 Q8P7P0	Q8p7p0 xanthomonas
14	44	53.7	306	2 Q69J37	Q69j37 oryza sativ
15	44	53.7	316	2 Q8A8P1	Q8a8p1 bacteroides
16	44	53.7	574	2 Q8SXM8	Q8sxm8 drosophila
17	44	53.7	599	1 ESRI MOUSE	P19785 mus musculu
18	44	53.7	600	1, ESRI RAT	P06211 rattus norv
19	44	53.7	607	2 Q9W3Z7	Q9w3z7 drosophila
20	43	52.4	162	1 RS16_MYCBO	P66436 mycobacteri
21	43	52.4	162	1 RS16_MYCTU	P66435 mycobacteri
22	43	52.4	289	2 Q71W13	Q71wi3 listeria mo
23	43	52.4	299	1 RL22 DROME	P50887 drosophila
24	43	52.4	304	2 Q7S9F3	Q7s9p3 neurospora
25	43	52.4	312	2 Q9UAN1	Q9uan1 drosophila
26	43	52.4	319	2 Q9N603	Q9n603 drosophila
27	43	52.4	319	2 Q9NG86	Q9ng86 drosophila
28	43	52.4	319	2 Q9NG87	Q9ng87 drosophila
29	43	52.4	319	2 Q9NG88	Q9ng88 drosophila
30	43	52.4	319	2 Q9NG89	Q9ng89 drosophila
31	43	52.4	319	2 Q9NG90	Q9ng90 drosophila

32	43	52.4	340	2 Q89J65	Q89j65 bradyrhizob
33	43	52.4	347	2 Q9JSP0	Q9jsp0 neisseria m
34	43	52.4	348	2 Q9K186	Q9k186 neisseria m
35	43	52.4	362	2 Q8EHS3	Q8ehs3 shewanella
36	43	52.4	413	2 Q83SA1	Q83sa1 shigella fl
37	43	52.4	421	1 TOLA ECOLI	P19934 escherichia
38	43	52.4	421	2 Q8FJT1	Q8fjt1 escherichia
39	43	52.4	442	1 BNB DROME	P29746 drosophila
40	43	52.4	508	2 Q6QUT5	Q6qut5 corynebacte
41	43	52.4	641	2 Q7SGF5	Q7sgf5 neurospora
42	43	52.4	759	2 Q6CCF1	Q6ccf1 yarrowia li
43	43	52.4	993	2 Q7S6Z8	Q7s6z8 neurospora
44	42.5	51.8	226	2 Q8BYX1	Q8byx1 mus musculu
45	42	51.2	112	2 Q6X3F6	Q6x3f6 pseudomonas

ALIGNMENTS

RESULT 1

Q96M46	PRELIMINARY;	PRT;	570 AA.
AC Q96M46;			
DT 01-DEC-2001 (Tremblrel. 19, Created)			
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)			
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)			
DE Hypothetical protein FLJ32830.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX NCBI_TaxID=9606;			
RN [1]			
RP SEQUENCE FROM N.A.			
RC TISSUE=Testis;			
RX PubMed=14702039; DOI=10.1038/ngl285;			
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,			
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,			
RA Sekine M., Obayashi M., Nishi T., Shibahara T., Tanaka T., Ishii S.,			
RA Yamamoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,			
RA Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M., Shiratori A.,			
RA Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,			
RA Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,			
RA Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M., Yamazaki M.,			
RA Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,			
RA Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,			
RA Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,			
RA Kanehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,			
RA Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,			
RA Musashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,			
RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,			
RA Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,			
RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,			
RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,			
RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,			
RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,			
RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,			
RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,			
RA Okitani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,			
RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Sasaki M.,			
RA Togashi T., Oyama M., Hata H., Watanabe M., Komatsu T.,			
RA Mizushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,			
RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,			
RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;			
RT "Complete sequencing and characterization of 21,243 full-length human			
RT cDNAs."			
RL Nat. Genet. 36:40-45(2004).			
DR EMBL; AK057392; BAB71466.1; -.			
DR InterPro; IPR008938; ARM.			
SQ SEQUENCE 570 AA; 65769 MW; 65BEEB6F244FC7E2 CRC64;			

Query Match 61.0%; Score 50; DB 2; Length 570;
Best Local Similarity 69.2%; Pred. No. 17;
Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY      2 PEKAKYEAYKAAA 14
      ||| |||||: |
Db      194 PEKVKEAYRTLA 206
      ||| |||||: |

RESULT 2
Q64CP3
ID Q64CP3 PRELIMINARY; PRT; 707 AA.
AC Q64CP3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN ORFNames=GZ1D1_21;
OS uncultured archaeon GZfos1D1.
OC Archaea; environmental samples.
OX NCBI_TaxID=286721;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15353801;
RA Hallam S.J., Putnam N., Preston C.M., Dettler J.C., Rokhsar D.,
RA Richardson P.M., DeLong E.F.;
RT "Reverse methanogenesis: testing the hypothesis with environmental
RT genomics.";
RL Science 305:1457-1462 (2004).
RN [2]
RP SEQUENCE FROM N.A.
RA Putnam N., Dettler J.C., Richardson P.M., Rokhsar D.;
RA Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL; AY714833; AAU82834.1; -.
KW Hypothetical protein.
SQ SEQUENCE 707 AA; 78670 MW; 104FE803EA51973D CRC64;

Query Match 58.5%; Score 48; DB 2; Length 707;
Best Local Similarity 70.6%; Pred. No. 43;
Matches 12; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAAAA 17
      ||| |||||: |
Db      643 AAELKSEAERAAAAA 659
      ||| |||||: |

RESULT 3
Q9JTN1
ID Q9JTN1 PRELIMINARY; PRT; 154 AA.
AC Q9JTN1;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMA1703.
GN OrderedLocusNames=NMA1703;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506 (2000).
DR EMBL; AL162756; CAB84931.1; -.
DR PIR; B81866; B81866.
DR HSSP; P44880; 1JMV.
DR GO; GO:0006950; P:response to stress; IEA.
```

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DR InterPro; IPR006015; Usp.
DR InterPro; IPR006016; UspA.
DR Pfam; PF00582; Usp; 1.
DR PRINTS; PR01438; UNVRSLSSTRESS.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 154 AA; 16552 MW; C9C4AFDDF521D064 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAAAA 16
      ||| |||||: |
Db      48 APEFLQHSYEAAAAVA 63
      ||| |||||: |

RESULT 4
Q9JYN4
ID Q9JYN4 PRELIMINARY; PRT; 154 AA.
AC Q9JYN4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein NMB1500.
GN OrderedLocusNames=NMB1500;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Massignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815 (2000).
DR EMBL; AE002499; AAF41856.1; -.
DR PIR; H81076; H81076.
DR HSSP; P44880; 1JMV.
DR TIGR; NMB1500; -.
DR GO; GO:0006950; P:response to stress; IEA.
DR InterPro; IPR006015; Usp.
DR InterPro; IPR006016; UspA.
DR Pfam; PF00582; Usp; 1.
DR PRINTS; PR01438; UNVRSLSSTRESS.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 154 AA; 16524 MW; CBAB524DF5221CAB CRC64;

Query Match 54.9%; Score 45; DB 2; Length 154;
Best Local Similarity 56.2%; Pred. No. 30;
Matches 9; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 APEKAKYEAYKAAAAA 16
      ||| |||||: |
Db      48 APEFLQHSYEAAAAVA 63
      ||| |||||: |

RESULT 5
RL19_AGR5
ID RL19_AGR5 STANDARD; PRT; 179 AA.
AC Q8UEZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
```

DE 50S ribosomal protein L19.
GN Name=rpL5; OrderedLocusNames=Atu2703, AGR_C 4900;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]

RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kuttyavin T., Levy R., Li M.-J., McClelland E., Romero P., Gordon D.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Perry M.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;

RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;

RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Quorllo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmiel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;

RT "Genome sequence of the plant pathogen and biotechnology agent

RT Agrobacterium tumefaciens C58.";

RL Science 294:2323-2328(2001).

CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).

CC -!- SIMILARITY: Belongs to the ribosomal protein L19P family.

CC -----
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CC -----

DR EMBL; AE09216; AAL43684.1; -

DR EMBL; AE08183; AAK88423.1; -

DR PIR; AF2908; AF2908.

DR PIR; F97683; F97683.

DR HAMAP; MF 00402; -; 1.

DR InterPro; IPR001857; Ribosomal L19.

DR Pfam; PF01245; Ribosomal L19; 1.

DR PRINTS; PR00061; RIBOSOMALL19.

DR ProDom; PD002979; Ribosomal L19; 1.

DR TIGRFAMs; TIGR01024; rpls_bact; 1.

DR PROSITE; PS01015; RIBOSOMAL_L19; 1.

KW Complete proteome; Ribosomal protein.

SQ SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

Query Match 54.9%; Score 45; DB 1; Length 179;

Best Local Similarity 64.7%; Pred. No. 35;

Matches 11; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17

Db 135 ABEKARLEAEKVAAQA 151

RESULT 6

Q9VFL4

ID Q9VFL4 PRELIMINARY; PRT; 300 AA.

AC Q9VFL4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG14840-PA (AT18408p).
GN ORFNames=CG14840;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazek R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolesley E.M.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,

RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;

RT "The genome sequence of Drosophila melanogaster.";

RL Science 287:2185-2195(2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,

RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,

RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,

RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;

RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila

RT melanogaster euchromatic genome sequence.";

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,

RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,

RA Ashburner M., Celniker S.E.;

RT "The transposable elements of the Drosophila melanogaster euchromatin:

RT a genomics perspective.";

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).

RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RN [7]
RP SEQUENCE FROM N.A.
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celniker S.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003704; AAF55038.1; -.
DR EMBL; AY089356; AAL90094.1; -.
DR IntAct; Q9VFL4; -.
DR FlyBase; FBgn0038217; CG14840.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 300 AA; 31262 MW; 67D1586E3044A8FC CRC64;

Query Match 54.9%; Score 45; DB 2; Length 300;
Best Local Similarity 71.4%; Pred. No. 57;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 16
Db 242 EKTQQAAYKACAA 255

RESULT 7
Q75GC3 ID Q75GC3 PRELIMINARY; PRT; 375 AA.
AC Q75GC3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Expressed protein, having alternative splicing products (Putative RNA
DE pol II accessory factor) (with alternative splicing).
GN Name=OSJNBb0031A14.2; Synonyms=OSJNBa0034D21.3;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.

RA Buell R.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.,
RA Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,
RA Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.,
RA Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,
RA Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J.,
RA White O., Salzberg S.L., Fraser C.M.;
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC145387; AAR88603.1; -.
DR EMBL; AC137991; AAS07322.1; -.
SQ SEQUENCE 375 AA; 42035 MW; 3B060F30076D2264 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 375;
Best Local Similarity 58.8%; Pred. No. 70;
Matches 10; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
Db 178 APSSARHEPSSAAAAA 194

RESULT 8
Q6D7F3 ID Q6D7F3 PRELIMINARY; PRT; 395 AA.
AC Q6D7F3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tola protein.
GN Name=tola; OrderedLocusNames=ECA1372;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110 (2004).
DR EMBL; BX950851; CAG74282.1; -.
DR InterPro; IPR010528; Tola.
DR Pfam; PF06519; Tola; 1.
KW Complete proteome.
SQ SEQUENCE 395 AA; 41698 MW; 2DB1DAA64E984199 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 395;
Best Local Similarity 70.6%; Pred. No. 74;
Matches 12; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 17
Db 203 AAETAKAEAKAAAEAA 219

RESULT 9
Q9V7U6 ID Q9V7U6 PRELIMINARY; PRT; 463 AA.
AC Q9V7U6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE CG6301-PA.
GN ORFNames=CG6301;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426065; PubMed=12537568;
RA Celniker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,
RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
melanogaster euchromatic genome sequence.";
RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426070; PubMed=12537573;
RA Kaminker J.S., Bergman C.M., Kronmiller B., Carlson J., Svirskas R.,
RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
RA Ashburner M., Celniker S.E.;
RT "The transposable elements of the Drosophila melanogaster euchromatin:
a genomics perspective.";
RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
systematic review.";
RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
RN [5]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A.
RG FlyBase;
RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE003805; AAF57947.2; -.
DR IntAct; Q9V7U6; -.
DR FlyBase; FBgn0034161; CG6301.
DR InterPro; IPR007999; DUF745.
DR Pfam; PF05335; DUF745; 1.
SQ SEQUENCE 463 AA; 49366 MW; 8D35569BEFB6EBC9 CRC64;

Query Match 54.9%; Score 45; DB 2; Length 463;
Best Local Similarity 71.4%; Pred. No. 86;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EKAKYEAYKAAAAA 16
DB 275 ETKQAAYKAAACA 288
||| ||||| ||
||| ||||| ||

RESULT 10
Q7M495 ID Q7M495 PRELIMINARY; PRT; 189 AA.
AC Q7M495;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Exoskeletal protein HACP202B (Fragment).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL Submitted (JUN-1997) to the PIR data bank.
DR PIR; S77935; S77935.
FT NON_TER 1 189
FT NON_TER 189 189
SQ SEQUENCE 189 AA; 20180 MW; 72A4EFC9C7ECFE9 CRC64;

Query Match 54.3%; Score 44.5; DB 2; Length 189;
Best Local Similarity 61.1%; Pred. No. 44;
Matches 11; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 APEKAK-YEAYKAAAAA 17
DB 9 AAEKARFFQAFKAAEAAA 26
|||: ::||| |||
|||: ::||| |||

RESULT 11
Q7M496 ID Q7M496 PRELIMINARY; PRT; 189 AA.
AC Q7M496;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Exoskeletal protein HACP202A (Fragment).
OS Homarus americanus (American lobster).

SQ SEQUENCE 306 AA; 32378 MW; A60288C9B77E8868 CRC64;
Query Match 53.7%; Score 44; DB 2; Length 306;
Best Local Similarity 68.8%; Pred. No. 84;
Matches 11; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PEKAKYEAYKAAAAA 17
| | | | : | | | | |
Db 122 PEKEAAKADKAAAAA 137

RESULT 15
Q8A8P1 PRELIMINARY; PRT; 316 AA.
AC Q8A8P1;
DT 01-JUN-2003 (TReMBLrel. 24, Created)
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Mobilization protein BmgA.
GN OrderedLocusNames=Btl126;
OS Bacteroides thetaiotaomicron.
OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Bacteroidaceae; Bacteroides.
OX NCBI_TaxID=818;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VPI-5482 / ATCC 29148;
RX MEDLINE=22550858; PubMed=12663928; DOI=10.1126/science.1080029;
RA Xu J., Bjursell M.K., Himrod J., Deng S., Carmichael L.K.,
RA Chiang H.C., Hooper L.V., Gordon J.I.;
RT "A genomic view of the human-Bacteroides thetaiotaomicron symbiosis."
RL Science 299:2074-2076(2003).
DR EMBL; AE016930; AAO76233.1; -.
DR InterPro; IPR005094; Relaxase.
DR Pfam; PF03432; Relaxase; 1.
KW Complete proteome.
SQ SEQUENCE 316 AA; 36130 MW; B63E149ACEDEC898 CRC64;

Query Match 53.7%; Score 44; DB 2; Length 316;
Best Local Similarity 56.2%; Pred. No. 86;
Matches 9; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 APEKAKYEAYKAAAAA 16
| | | | | : | | | |
Db 171 ASEKVKYEIYRAVKEA 186

Search completed: March 31, 2005, 02:41:09
Job time : 93.3065 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds
(without alignments)
65.338 Million cell updates/sec

Title: US-10-056-583A-91
Perfect score: 76
Sequence: 1 EKPKEAYKAAAPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	76	100.0	15	5	ABP52297	Abp52297 HLA-DR2 m
2	73	96.1	15	5	ABP52291	Abp52291 HLA-DR2 m
3	70	92.1	15	5	ABP52304	Abp52304 HLA-DR2 m
4	69	90.8	15	5	ABP52299	Abp52299 HLA-DR2 m
5	68	89.5	17	5	ABP52303	Abp52303 HLA-DR2 m
6	67	88.2	15	5	ABP52290	Abp52290 HLA-DR2 m
7	67	88.2	15	5	ABP52292	Abp52292 HLA-DR2 m
8	64	84.2	17	5	ABP52302	Abp52302 HLA-DR2 m
9	63	82.9	15	5	ABP52300	Abp52300 HLA-DR2 m
10	63	82.9	15	5	ABP52305	Abp52305 HLA-DR2 m
11	57	75.0	15	5	ABP52271	Abp52271 HLA-DR2 m
12	57	75.0	15	5	ABP52289	Abp52289 HLA-DR2 m
13	57	75.0	15	5	ABP52298	Abp52298 HLA-DR2 m
14	57	75.0	17	5	ABP52294	Abp52294 HLA-DR2 m
15	57	75.0	17	5	ABP52296	Abp52296 HLA-DR2 m
16	57	75.0	19	5	ABP52295	Abp52295 HLA-DR2 m
17	56	73.7	15	5	ABP52301	Abp52301 HLA-DR2 m
18	53	69.7	15	5	ABP52293	Abp52293 HLA-DR2 m
19	53	69.7	781	8	ADN60395	Adn60395 B. lichen
20	53	69.7	781	8	ADN60505	Adn60505 B. lichen
21	53	69.7	781	8	ADN60519	Adn60519 B. lichen
22	51	67.1	15	5	ABP52270	Abp52270 HLA-DR2 m
23	51	67.1	15	5	ABP52272	Abp52272 HLA-DR2 m
24	47	61.8	15	5	ABP52263	Abp52263 HLA-DR2 m
25	46	60.5	299	4	ABB63276	Abb63276 Drosophil

26	46	60.5	299	8	ADS96704	Ads96704 Drosophil
27	45	59.2	15	5	ABP52264	Abp52264 HLA-DR2 m
28	45	59.2	15	5	ABP52267	Abp52267 HLA-DR2 m
29	45	59.2	15	5	ABP52259	Abp52259 HLA-DR2 m
30	45	59.2	15	5	ABP52257	Abp52257 HLA-DR2 m
31	44	57.9	377	6	ABU23345	Abu23345 Protein e
32	43	56.6	15	5	ABP52265	Abp52265 HLA-DR2 m
33	43	56.6	336	6	ABP79775	Abp79775 N. gonorr
34	43	56.6	336	6	ABU38057	Abu38057 Protein e
35	43	56.6	336	6	ABU37170	Abu37170 Protein e
36	43	56.6	336	8	ADP08309	Adp08309 Neisseria
37	43	56.6	572	4	ABB59072	Abb59072 Drosophil
38	42	55.3	15	5	ABP52254	Abp52254 HLA-DR2 m
39	42	55.3	15	5	ABP52255	Abp52255 HLA-DR2 m
40	42	55.3	15	5	ABP52240	Abp52240 HLA-DR2 m
41	42	55.3	15	5	ABP52253	Abp52253 HLA-DR2 m
42	42	55.3	15	5	ABP52251	Abp52251 HLA-DR2 m
43	42	55.3	15	5	ABP52241	Abp52241 HLA-DR2 m
44	42	55.3	15	5	ABP52249	Abp52249 HLA-DR2 m
45	42	55.3	15	5	ABP52239	Abp52239 HLA-DR2 m

ALIGNMENTS

RESULT 1
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX AC ABP52297;
XX DT 16-OCT-2002 (first entry)
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX OS Homo sapiens.
XX OS Synthetic.
XX PN WO200259143-A2.
XX PD 01-AUG-2002.
XX PF 24-JAN-2002; 2002WO-US002071.
XX PR 24-JAN-2001; 2001US-0263569P.
XX PA (HARD) HARVARD COLLEGE.
XX PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX PS Claim 28; Page 39; 54pp; English.
XX CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 76; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.4e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
Db 1 EKPKFEAYKAAAPAA 15

RESULT 2
ABP52291
ID ABP52291 standard; peptide; 15 AA.

XX AC ABP52291;
XX DT 16-OCT-2002 (first entry)
XX DE HLA-DR2 molecule binding peptide SEQ ID NO:85.
XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.
XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX PS WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
XX invention

SQ Sequence 15 AA;

Query Match 96.1%; Score 73; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.3e-05;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
Db 1 EKPKFEAYKAAAPAA 15

RESULT 3
ABP52304

ID ABP52304 standard; peptide; 15 AA.

XX AC ABP52304;

XX DT 16-OCT-2002 (first entry)

XX DE HLA-DR2 molecule binding peptide SEQ ID NO:98.

XX KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.

XX OS Homo sapiens.
XX OS Synthetic.

XX PN WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX PS WPI; 2002-608439/65.

XX PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
XX invention

SQ Sequence 15 AA;

Query Match 92.1%; Score 70; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.00013;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15

```

Db      | |||||
        1 EAPKFEAYKAAAPAA 15

RESULT 4
ABP52299
ID      ABP52299 standard; peptide; 15 AA.
XX
AC      ABP52299;
XX
DT      16-OCT-2002 (first entry)
XX
DE      HLA-DR2 molecule binding peptide SEQ ID NO:93.
XX
KW      Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW      HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW      immune response; antiinflammatory; neuroprotective; proliferation;
KW      MHC class II protein inhibitor; demyelinating disease; inhibition;
KW      post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW      anti-tumour necrosis factor agent.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200259143-A2.
XX
PD      01-AUG-2002.
XX
PF      Homo sapiens.
OS      Synthetic.
XX
PN      WO200259143-A2.
XX
PD      01-AUG-2002.
XX
PF      24-JAN-2002; 2002WO-US002071.
XX
PR      24-JAN-2001; 2001US-0263569P.
XX
PA      (HARD ) HARVARD COLLEGE.
XX
PI      Strominger JL, Fridkis-Hareli M;
XX
WPI; 2002-608439/65.
XX
New compositions comprising synthetic peptides in complex with a major
histocompatibility complex class II HLA-DR2 protein, useful for treating a
demyelinating disease, e.g. multiple sclerosis, or post-viral
encephalomyelitis.
XX
Claim 28; Page 39; 54pp; English.
XX
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complex (MHC) class II HLA-DR2 protein is involved in modulating an
immune response. (I) has antiinflammatory and neuroprotective activities,
and can be used as a MHC class II protein inhibitor. The compositions
comprising the peptides are useful for treating demyelinating diseases
such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
demyelinating condition, and a side effect of administering an anti-
tumour necrosis factor agents. The peptide further inhibits proliferation
of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
ABP52305 represent peptides used in the exemplification of the present
invention
XX
SQ      Sequence 15 AA;
Query Match          90.8%; Score 69; DB 5; Length 15;
Best Local Similarity 93.3%; Pred. No. 0.0002;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
        |||||
Db      1 EKPKEAYKAAAPAA 15

RESULT 5
ABP52303
ID      ABP52303 standard; peptide; 17 AA.
XX
AC      ABP52303;
XX
DT      16-OCT-2002 (first entry)
XX
DE      HLA-DR2 molecule binding peptide SEQ ID NO:84.
XX
KW      Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW      HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW      immune response; antiinflammatory; neuroprotective; proliferation;
KW      MHC class II protein inhibitor; demyelinating disease; inhibition;
KW      post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW      anti-tumour necrosis factor agent.
XX
OS      Homo sapiens.
OS      Synthetic.
XX
PN      WO200259143-A2.
XX
PD      01-AUG-2002.
XX
PF      Homo sapiens.
OS      Synthetic.
XX
PN      WO200259143-A2.
XX
PD      01-AUG-2002.
XX
PF      24-JAN-2002; 2002WO-US002071.
XX
PR      24-JAN-2001; 2001US-0263569P.
XX
PA      (HARD ) HARVARD COLLEGE.
XX
PI      Strominger JL, Fridkis-Hareli M;
XX
WPI; 2002-608439/65.
XX
New compositions comprising synthetic peptides in complex with a major
histocompatibility complex class II HLA-DR2 protein, useful for treating a
demyelinating disease, e.g. multiple sclerosis, or post-viral
encephalomyelitis.
XX
Claim 28; Page 39; 54pp; English.
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comprising the peptides are useful for treating demyelinating diseases
such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
demyelinating condition, and a side effect of administering an anti-
tumour necrosis factor agents. The peptide further inhibits proliferation
of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
ABP52305 represent peptides used in the exemplification of the present
invention
XX
SQ      Sequence 17 AA;
Query Match          89.5%; Score 68; DB 5; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.0003;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
        |||||
Db      3 EKPKEAYKAAAPAA 17

RESULT 6
ABP52290
ID      ABP52290 standard; peptide; 15 AA.
XX
AC      ABP52290;
XX
DT      16-OCT-2002 (first entry)
XX
DE      HLA-DR2 molecule binding peptide SEQ ID NO:84.
XX
```

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
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CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 88.2%; Score 67; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00042;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKPKEAYKAAAPAA 15
Db 1 EAPKYEAYKAAAPAA 15
RESULT 7
ABP52292
ID ABP52292 standard; peptide; 15 AA.
XX
AC ABP52292;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:86.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX

OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
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CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
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CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 88.2%; Score 67; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00042;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKPKEAYKAAAPAA 15
Db 1 EAPKYEAYKAAAPAA 15
RESULT 8
ABP52302
ID ABP52302 standard; peptide; 17 AA.
XX
AC ABP52302;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX

PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
XX WPI; 2002-608439/65.
XX
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
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CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 84.2%; Score 64; DB 5; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0015;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15
||| ||||:|||||||
Db 3 EKAKFEAFKAAAPAA 17

RESULT 9
ABP52300
ID ABP52300 standard; peptide; 15 AA.
XX
AC ABP52300;
XX
DT 16-OCT-2002 (first entry).
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:94.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;

Query Match 82.9%; Score 63; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0019;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15
||| ||||:|||||||
Db 1 EKPKEEAFKAAAPAA 15

RESULT 10
ABP52305
ID ABP52305 standard; peptide; 15 AA.
XX
AC ABP52305;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:99.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide

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CC residues. The complex of the peptide with a major histocompatibility

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CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

XX Query Match 82.9%; Score 63; DB 5; Length 15;

XX Best Local Similarity 86.7%; Pred. No. 0.0019;

XX Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15

DB 1 EAPKVEAYKAAAPAA 15

RESULT 11

ABP52271

ID ABP52271 standard; peptide; 15 AA.

XX

AC ABP52271;

XX

DT 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:65.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

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PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

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CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

XX Query Match 75.0%; Score 57; DB 5; Length 15;

XX Best Local Similarity 80.0%; Pred. No. 0.019;

XX Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15

DB 1 EKAKYEAYKAAAPAA 15

RESULT 12

ABP52289

ID ABP52289 standard; peptide; 15 AA.

XX

AC ABP52289;

XX

DT 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:83.

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

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PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

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CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 75.0%; Score 57; DB 5; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.019;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
Db 1 EAPAYKAYKAAAPAA 15

RESULT 13
ABP52298
ID ABP52298 standard; peptide; 15 AA.
XX
AC ABP52298;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:92.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
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PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
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PS Claim 28; Page 39; 54pp; English.
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CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 75.0%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.019;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
Db 1 EKAKYEAYKAAAPAA 15

RESULT 14
ABP52294
ID ABP52294 standard; peptide; 17 AA.
XX
AC ABP52294;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:88.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
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CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
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CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 75.0%; Score 57; DB 5; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches. 2; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
Db 3 EKAKYEAYKAAAPAA 17

RESULT 15
ABP52296
ID ABP52296 standard; peptide; 17 AA.
XX
AC ABP52296;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:90.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;

Query Match 75.0%; Score 57; DB 5; Length 17;
Best Local Similarity 80.0%; Pred. No. 0.021;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPA 15
|||:|||||||
Db 1 EKAKYEAYKAAAAA 15

Search completed: March 31, 2005, 02:35:28
Job time : 89.7903 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds
(without alignments)
48.718 Million cell updates/sec

Title: US-10-056-583A-91
Perfect score: 76
Sequence: 1 EKPKEAYKAAAPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	52.6	2471	1 US-08-185-432-16	Sequence 16, Appl
2	40	52.6	2471	1 US-08-083-590A-19	Sequence 19, Appl
3	40	52.6	2471	3 US-08-532-384-19	Sequence 19, Appl
4	40	52.6	2471	4 US-08-899-232-1	Sequence 1, Appli
5	40	52.6	2471	4 US-09-121-457-1	Sequence 1, Appli
6	39	51.3	75	4 US-09-513-999C-5101	Sequence 5101, Ap
7	39	51.3	222	4 US-09-949-016-9547	Sequence 9547, Ap
8	39	51.3	243	4 US-09-489-039A-7214	Sequence 7214, Ap
9	39	51.3	297	4 US-09-252-991A-18932	Sequence 18932, A
10	39	51.3	314	3 US-09-004-838-14	Sequence 14, Appl
11	39	51.3	469	4 US-09-252-991A-27869	Sequence 27869, A
12	39	51.3	1402	3 US-09-004-838-11	Sequence 11, Appl
13	38	50.0	66	4 US-09-902-540-16512	Sequence 16512, A
14	38	50.0	203	4 US-09-248-796A-20648	Sequence 20648, A
15	38	50.0	260	4 US-09-248-796A-17592	Sequence 17592, A
16	38	50.0	287	3 US-09-105-697-7	Sequence 7, Appli
17	38	50.0	287	3 US-09-105-697-8	Sequence 8, Appli
18	38	50.0	288	3 US-09-105-697-3	Sequence 3, Appli
19	38	50.0	291	3 US-09-105-697-4	Sequence 4, Appli
20	38	50.0	291	3 US-09-105-697-5	Sequence 5, Appli
21	38	50.0	291	3 US-09-105-697-6	Sequence 6, Appli
22	38	50.0	435	4 US-09-949-016-7245	Sequence 7245, Ap
23	38	50.0	490	4 US-10-029-180-76	Sequence 76, Appl
24	38	50.0	499	4 US-09-902-540-15480	Sequence 15480, A
25	38	50.0	576	4 US-09-543-681A-7747	Sequence 7747, Ap
26	38	50.0	830	1 US-07-977-434-6	Sequence 6, Appli
27	38	50.0	830	1 US-08-458-819-6	Sequence 6, Appli

28	38	50.0	830	5 PCT-US91-07035-6	Sequence 6, Appli
29	38	50.0	831	1 US-08-073-384C-5	Sequence 5, Appli
30	38	50.0	831	1 US-08-254-359A-5	Sequence 5, Appli
31	38	50.0	831	1 US-08-483-043-5	Sequence 5, Appli
32	38	50.0	831	1 US-08-481-238-5	Sequence 5, Appli
33	38	50.0	831	2 US-08-471-066B-5	Sequence 5, Appli
34	38	50.0	831	2 US-08-484-956-5	Sequence 5, Appli
35	38	50.0	831	2 US-08-757-653-5	Sequence 5, Appli
36	38	50.0	831	2 US-08-599-491-5	Sequence 5, Appli
37	38	50.0	831	2 US-08-756-386-5	Sequence 5, Appli
38	38	50.0	831	2 US-08-823-516-5	Sequence 5, Appli
39	38	50.0	831	3 US-08-682-853A-5	Sequence 5, Appli
40	38	50.0	831	3 US-08-759-038-5	Sequence 5, Appli
41	38	50.0	831	3 US-08-758-314-5	Sequence 5, Appli
42	38	50.0	831	3 US-09-350-309-5	Sequence 5, Appli
43	38	50.0	831	3 US-08-520-946-5	Sequence 5, Appli
44	38	50.0	831	4 US-09-684-938-5	Sequence 5, Appli
45	38	50.0	831	4 US-09-308-825A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-185-432-16
; Sequence 16, Application US/08185432
; Patent No. 5750652
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Busseau, Isabelle
; APPLICANT: Diederich, Robert J.
; APPLICANT: Xu, Tian
; APPLICANT: Matsuno, Kenji
; TITLE OF INVENTION: DELTEX PROTEINS, NUCLEIC ACIDS, AND
; TITLE OF INVENTION: ANTIBODIES, AND RELATED METHODS AND COMPOSITIONS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PENNIE & EDMONDS
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/185,432
; FILING DATE: 21-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-006
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-8864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-185-432-16

Query Match 52.6%; Score 40; DB 1; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 14

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Db      850 ESPNFESYTCLCAP 863

RESULT 2
US-08-083-590A-19
; Sequence 19, Application US/08083590A
; Patent No. 5786158
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 5786158ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/083,590A
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mirock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 7326-015
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2471 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-083-590A-19

Query Match      52.6%; Score 40; DB 1; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 EKPKFEAYKAAAP 14
Db      850 ESPNFESYTCLCAP 863

RESULT 3
US-08-532-384-19
; Sequence 19, Application US/08532384
; Patent No. 6083904
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S. et al.
; TITLE OF INVENTION: Therapeutic And Diagnostic Methods
; TITLE OF INVENTION: And Compositions Based On No. 6083904ch Proteins And
; TITLE OF INVENTION: Nucleic Acids
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036

Query Match      52.6%; Score 40; DB 1; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 EKPKFEAYKAAAP 14
Db      850 ESPNFESYTCLCAP 863

RESULT 4
US-08-899-232-1
; Sequence 1, Application US/08899232
; Patent No. 6436650
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, Spyridon
; APPLICANT: Qi, Huilin
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-046
; CURRENT APPLICATION NUMBER: US/08/899,232
; CURRENT FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-899-232-1

Query Match      52.6%; Score 40; DB 4; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      1 EKPKFEAYKAAAP 14
Db      850 ESPNFESYTCLCAP 863

RESULT 5
US-09-121-457-1
; Sequence 1, Application US/09121457
; Patent No. 6692919
; GENERAL INFORMATION:
; APPLICANT: Artavanis-Tsakonas, S.
; APPLICANT: Qi, H.
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; APPLICANT: Rand, M.
; TITLE OF INVENTION: ACTIVATED FORMS OF NOTCH AND METHODS BASED THEREON
; FILE REFERENCE: 7326-073
; CURRENT APPLICATION NUMBER: US/09/121,457
; CURRENT FILING DATE: 1998-07-23
; EARLIER APPLICATION NUMBER: 08/899,232
; EARLIER FILING DATE: 1997-07-23
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 2471
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-121-457-1

Query Match      52.6%; Score 40; DB 4; Length 2471;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAP 14
      |||||
Db      850 ESPNFESYTCCLCAP 863

RESULT 6
US-09-513-999C-5101
; Sequence 5101, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 5101
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-513-999C-5101

Query Match      51.3%; Score 39; DB 4; Length 75;
Best Local Similarity 64.3%; Pred. No. 11;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 KPKFEAYKAAAP 15
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Db      7 EPKKEAAKPAPAPA 20

RESULT 7
US-09-949-016-9547
; Sequence 9547, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
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; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9547
; LENGTH: 222
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9547

Query Match      51.3%; Score 39; DB 4; Length 222;
Best Local Similarity 64.3%; Pred. No. 38;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 KPKFEAYKAAAP 15
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Db      32 EPKKEAAKPAPAPA 45

RESULT 8
US-09-489-039A-7214
; Sequence 7214, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 7214
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-7214

Query Match      51.3%; Score 39; DB 4; Length 243;
Best Local Similarity 58.3%; Pred. No. 42;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 PKPEAYKAAAP 14
      |||
Db      122 PEFTAFSAATP 133

RESULT 9
US-09-252-991A-18932
; Sequence 18932, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18932
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18932

Query Match      51.3%; Score 39; DB 4; Length 297;
Best Local Similarity 46.7%; Pred. No. 52;
Matches 7; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAP 15
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Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAA 11
 Db 515 EKPKIEREAS 525

RESULT 13

US-09-902-540-16512
 ; Sequence 16512, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 16512.
 ; LENGTH: 66
 ; TYPE: PRT
 ; ORGANISM: Myxococcus xanthus
 US-09-902-540-16512

Query Match 50.0%; Score 38; DB 4; Length 66;
 Best Local Similarity 72.7%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 FEAYKAAAPA 15
 Db 48 FEIYAALAAPA 58

RESULT 14

US-09-248-796A-20648
 ; Sequence 20648, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 20648
 ; LENGTH: 203
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 ; FEATURE:
 ; NAME/KEY: UNSURE
 ; LOCATION: (11)
 ; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unkno
 US-09-248-796A-20648

Query Match 50.0%; Score 38; DB 4; Length 203;
 Best Local Similarity 77.8%; Pred. No. 51;
 Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 KPKEAYKA 10
 Db 42 KPKEPTKA 50

RESULT 15

US-09-248-796A-17592
 ; Sequence 17592, Application US/09248796A
 ; Patent No. 6747137
 ; GENERAL INFORMATION:
 ; APPLICANT: Keith Weinstock et al
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAI
 ; FILE REFERENCE: 107196.132
 ; CURRENT APPLICATION NUMBER: US/09/248,796A
 ; CURRENT FILING DATE: 1999-02-12
 ; PRIOR APPLICATION NUMBER: US 60/074,725
 ; PRIOR FILING DATE: 1998-02-13
 ; PRIOR APPLICATION NUMBER: US 60/096,409
 ; PRIOR FILING DATE: 1998-08-13
 ; NUMBER OF SEQ ID NOS: 28208
 ; SEQ ID NO 17592
 ; LENGTH: 260
 ; TYPE: PRT
 ; ORGANISM: Candida albicans
 US-09-248-796A-17592

Query Match 50.0%; Score 38; DB 4; Length 260;
 Best Local Similarity 87.5%; Pred. No. 67;
 Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PKFEAYKA 10
 Db 112 PKFEYKA 119

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 Job time : 23.9839 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds
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Title: US-10-056-583A-91
Perfect score: 76
Sequence: 1 EKPKFEAYKAAAPAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	76	100.0	15	14	US-10-056-583-91 Sequence 91, Appl
2	73	96.1	15	14	US-10-056-583-85 Sequence 85, Appl
3	70	92.1	15	14	US-10-056-583-98 Sequence 98, Appl
4	69	90.8	15	14	US-10-056-583-93 Sequence 93, Appl
5	68	89.5	17	14	US-10-056-583-97 Sequence 97, Appl
6	67	88.2	15	14	US-10-056-583-84 Sequence 84, Appl
7	67	88.2	15	14	US-10-056-583-86 Sequence 86, Appl
8	64	84.2	17	14	US-10-056-583-96 Sequence 96, Appl
9	63	82.9	15	14	US-10-056-583-94 Sequence 94, Appl
10	63	82.9	15	14	US-10-056-583-99 Sequence 99, Appl
11	57	75.0	15	14	US-10-056-583-65 Sequence 65, Appl
12	57	75.0	15	14	US-10-056-583-83 Sequence 83, Appl
13	57	75.0	17	14	US-10-056-583-88 Sequence 88, Appl

14	57	75.0	17	14	US-10-056-583-90	Sequence 90, Appl
15	57	75.0	19	14	US-10-056-583-89	Sequence 89, Appl
16	56	73.7	15	14	US-10-056-583-95	Sequence 95, Appl
17	53	69.7	15	14	US-10-056-583-87	Sequence 87, Appl
18	51	67.1	15	14	US-10-056-583-64	Sequence 64, Appl
19	51	67.1	15	14	US-10-056-583-66	Sequence 66, Appl
20	51	67.1	15	14	US-10-056-583-92	Sequence 92, Appl
21	47	61.8	15	14	US-10-056-583-57	Sequence 57, Appl
22	45	59.2	15	14	US-10-056-583-51	Sequence 51, Appl
23	45	59.2	15	14	US-10-056-583-53	Sequence 53, Appl
24	45	59.2	15	14	US-10-056-583-58	Sequence 58, Appl
25	45	59.2	15	14	US-10-056-583-61	Sequence 61, Appl
26	44	57.9	377	15	US-10-282-122A-51269	Sequence 51269, A
27	43	56.6	15	14	US-10-056-583-59	Sequence 59, Appl
28	43	56.6	336	15	US-10-282-122A-65094	Sequence 65094, A
29	43	56.6	336	15	US-10-282-122A-65981	Sequence 65981, A
30	42.5	55.9	316	16	US-10-767-701-45123	Sequence 45123, A
31	42	55.3	15	14	US-10-056-583-33	Sequence 33, Appl
32	42	55.3	15	14	US-10-056-583-34	Sequence 34, Appl
33	42	55.3	15	14	US-10-056-583-35	Sequence 35, Appl
34	42	55.3	15	14	US-10-056-583-43	Sequence 43, Appl
35	42	55.3	15	14	US-10-056-583-45	Sequence 45, Appl
36	42	55.3	15	14	US-10-056-583-47	Sequence 47, Appl
37	42	55.3	15	14	US-10-056-583-48	Sequence 48, Appl
38	42	55.3	15	14	US-10-056-583-49	Sequence 49, Appl
39	41	53.9	15	14	US-10-056-583-38	Sequence 38, Appl
40	41	53.9	15	14	US-10-056-583-55	Sequence 55, Appl
41	41	53.9	15	14	US-10-056-583-56	Sequence 56, Appl
42	41	53.9	15	14	US-10-056-583-62	Sequence 62, Appl
43	41	53.9	15	14	US-10-056-583-63	Sequence 63, Appl
44	41	53.9	317	15	US-10-310-154-522	Sequence 522, App
45	41	53.9	319	16	US-10-767-701-47195	Sequence 47195, A

ALIGNMENTS

RESULT 1
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

Query Match 100.0%; Score 76; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.5e-06;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
| | | | | | | | | | | | | | |
Db 1 EKPKFEAYKAAAPAA 15

RESULT 2
US-10-056-583-85

```
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85
```

```
Query Match          96.1%; Score 73; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 8.2e-06;
Matches 14; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 EKPKEAYKAAAPAA 15
Db 1 EKPKEAYKAAAPAA 15
```

```
RESULT 3
US-10-056-583-98
; Sequence 98, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 98
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-98
```

```
Query Match          92.1%; Score 70; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 2.7e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EKPKEAYKAAAPAA 15
Db 1 EAPKEAYKAAAPAA 15
```

```
RESULT 4
US-10-056-583-93
; Sequence 93, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 93
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-93
```

```
Query Match          90.8%; Score 69; DB 14; Length 15;
Best Local Similarity 93.3%; Pred. No. 4.1e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EKPKEAYKAAAPAA 15
Db 1 EKPKEAYKAAAPAA 15
```

```
RESULT 5
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97
```

```
Query Match          89.5%; Score 68; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 6.9e-05;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 1 EKPKEAYKAAAPAA 15
Db 3 EAPKEAYKAAAPAA 17
```

```
RESULT 6
US-10-056-583-84
; Sequence 84, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```

```
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 84
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-84

Query Match      88.2%; Score 67; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 9e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
Db      1 EAPKYEAYKAAAPAA 15

RESULT 7
US-10-056-583-86
; Sequence 86, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-86

Query Match      88.2%; Score 67; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 9e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
Db      1 EAPKYEAYKAAAPAA 15

RESULT 8
US-10-056-583-96
; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 86
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96

Query Match      88.2%; Score 67; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 9e-05;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
Db      1 EAPKYEAYKAAAPAA 15

RESULT 9
US-10-056-583-94
; Sequence 94, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 94
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-94

Query Match      82.9%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00044;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
Db      1 EKPKEAYKAAAPAA 15

RESULT 10
US-10-056-583-99
; Sequence 99, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99

Query Match      82.9%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00044;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      1 EKPKEAYKAAAPAA 15
Db      1 EKPKEAYKAAAPAA 15
```

OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-99

Query Match 82.9%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred.No. 0.00044;
Matches 13; Conservative 0; Mismatches 2; Indels

Qy 1 EKPKFEAYKAAAAA 15
| | | | | | | | | |
Db 1 EAPKVEAYKAAAAA 15

```

RESULT 11
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-65

```

Query Match 75.0%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0048;
Matches 12; Conservative 1; Mismatches 2; Indels

Qy 1 EKPFEEAYKAAAAA 15
|||:|||||
Db 1 EKAYEAYKAAAAAA 15

```

RESULT 12
US-10-056-583-83
; Sequence 83, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Maasha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 83
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized
US-10-056-583-83

```

Query Match	75.0%	Score 57;	DB 14;	Length 15;
Best Local Similarity	73.3%	Pred. No. 0.0048;		

Matches	11;	Conservative	2;	Mismatches	2;	Indels	0;	Gaps	0;
---------	-----	--------------	----	------------	----	--------	----	------	----

Qy 1 EKPKFEAYKAAAAPA 15
| | : | | | | | |
Db 1 EPAYKAYKAAAAPA 15

```

RESULT 13
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88

```

Query Match	75.0%;	Score 57;	DB 14;	Length 17;
Best Local Similarity	80.0%;	Pred. No. 0.0056;		
Matches 12: Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 EKPKFEAYKAAAPA 15
|||:|||||
pb 3 EKAKYEAYKAAAAA 17

```

RESULT 14
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90

```

Query Match	75.0%	Score 57;	DB 14;	Length 17;
Best Local Similarity	80.0%;	Pred. No. 0.0056;		
Matches 12; Conservative	1;	Mismatches 2;	Indels 0;	Gaps 0;

Qy 1 EKPKFEAYKAAAAA 15
|||:|||||
Db 1 EKAKYEAYKAAAAAA 15

RESULT 15
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89

Query Match 75.0%; Score 57; DB 14; Length 19;
Best Local Similarity 80.0%; Pred. No. 0.0063;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 15
|||:|||||||
Db 3 EKAYEAYKAAAAA 17

Search completed: March 31, 2005, 02:48:48
Job time : 66.5323 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds
(without alignments)
80.614 Million cell updates/sec

Title: US-10-056-583A-91
Perfect score: 76
Sequence: 1 EKPKEAYKAAAPA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79: *
1: Pirl: *
2: pirl2: *
3: pirl3: *
4: pirl4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	57.9	193	1 MOMS4E	myosin alkali ligh
2	43	56.6	306	2 G96014	hypothetical prote
3	43	56.6	336	2 B81081	tryptophanyl-trNA
4	43	56.6	336	2 E81863	tryptophan-trNA li
5	43	56.6	389	2 G87332	hypothetical prote
6	42.5	55.9	316	2 T14643	1-aminocyclopropan
7	42	55.3	270	2 T31225	traF protein homol
8	42	55.3	554	2 S68365	(+)-delta-cadinene
9	42	55.3	554	2 S68366	(+)-delta-cadinene
10	41	53.9	185	1 MOCH4E	myosin alkali ligh
11	41	53.9	193	1 MORT4E	myosin alkali ligh
12	41	53.9	194	2 T14644	1-aminocyclopropan
13	41	53.9	200	2 T48130	hypothetical prote
14	41	53.9	216	2 AG3508	transporter BMEI20
15	41	53.9	398	2 T21061	hypothetical prote
16	40	52.6	321	2 T07922	probable 1-aminocy
17	40	52.6	461	2 AI3358	pyruvate dehydroge
18	40	52.6	765	2 T15447	hypothetical prote
19	40	52.6	891	2 AC3384	ribonuclease E / z
20	39	51.3	73	2 S40015	phd protein - phag
21	39	51.3	114	2 G81353	hypothetical prote
22	39	51.3	168	2 A45943	vitelline membrane
23	39	51.3	197	1 MOHU4E	myosin alkali ligh
24	39	51.3	215	2 AG3392	maleylpyruvate iso
25	39	51.3	239	1 C44954	fumarate reductase
26	39	51.3	310	2 T09733	1-aminocyclopropan
27	39	51.3	321	2 T02754	probable 1-aminocy
28	39	51.3	334	1 DEQYG	glyceraldehyde-3-p
29	39	51.3	334	2 E75153	glyceraldehyde 3-p

30	39	51.3	334	2 G71194	probable glycerald
31	39	51.3	337	1 C70473	phosphate-binding
32	39	51.3	465	2 D83598	probable zinc prot
33	39	51.3	538	2 S54015	C-22 sterol desatu
34	39	51.3	586	2 T29657	hypothetical prote
35	39	51.3	656	2 AE1479	probable cell surf
36	39	51.3	810	2 C95401	probable oxidoredu
37	38.5	50.7	906	2 T00039	hypothetical prote
38	38	50.0	50	2 G97151	hypothetical prote
39	38	50.0	179	2 F97683	50S ribosomal prot
40	38	50.0	179	2 AF2908	50S ribosomal prot
41	38	50.0	188	2 I50145	homeotic protein H
42	38	50.0	269	2 E86691	ABC transporter AT
43	38	50.0	289	2 A43562	homeotic protein H
44	38	50.0	308	2 T10817	1-aminocyclopropan
45	38	50.0	320	2 B86255	hypothetical prote

ALIGNMENTS

RESULT 1

MOMS4E
myosin alkali light chain 4, embryonic and atrial - mouse
N;Alternate names: MLC1A, MLC1emb; myosin L1 catalytic light chain, atrial
C;Species: Mus musculus (house mouse)
C;Date: 31-Mar-1990 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
C;Accession: A31114; S01944
R;Barton, P.J.R.; Robert, B.; Cohen, A.; Garner, I.; Sassoon, D.; Weydert, A.; Buckingham
J. Biol. Chem. 263, 12669-12676, 1988
A;Title: Structure and sequence of the myosin alkali light chain gene expressed in adult
A;Reference number: A31114; MUID:88315068; PMID:2842339
A;Accession: A31114
A;Molecule type: DNA
A;Residues: 1-193 <BAR>
A;Cross-references: UNIPROT:P09541; GB:M20772; GB:J03932; GB:M19435; NID:G199731; PIDN:A
R;Cohen, A.; Barton, P.J.R.; Robert, B.; Garner, I.; Alonso, S.; Buckingham, M.E.
Nucleic Acids Res. 16, 10037-10052, 1988
A;Title: Promoter analysis of myosin alkali light chain genes expressed in mouse striate
A;Reference number: S01944; MUID:89057447; PMID:3194193
A;Accession: S01944
A;Molecule type: DNA
A;Residues: 1-41 <COH>
A;Cross-references: EMBL:X12971; NID:G53138; PIDN:CAA31414.1; PID:G53139
C;Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet

C;Genetics:
A;Introns: 41/3; 51/1; 101/1; 159/1; 185/1
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contrac
F;47-81/Domain: calmodulin repeat homology <EF1>
F;126-158/Domain: calmodulin repeat homology <EF3>
F;161-193/Domain: calmodulin repeat homology <EF4>

Query Match 57.9%; Score 44; DB 1; Length 193;
Best Local Similarity 71.4%; Pred. No. 4;
Matches 10; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKFEAYKAAAPA 15

Db 7 EPKKEAKPAAAPA 20

RESULT 2

G96014
hypothetical protein [imported] - Sinorhizobium meliloti (strain 1021) magaplasamid pSymB
C;Species: Sinorhizobium meliloti
C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
C;Accession: G96014
R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
A;Title: The complete sequence of the 1,683-kb pSymB megaplasamid from the N2-fixing endo
A;Reference number: A95842; MUID:21396508; PMID:11481431
A;Accession: G96014

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-306 <KUR>
A;Cross-references: UNIPROT:Q92TW2; GB:AL591985; PIDN:CAC49783.1; PID:g15141270; GSPDB:G15141270
A;Experimental source: strain 1021, megaplasmid pSymB
R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler, R.; Gaudet, L.; Hyman, R.W.; Jones, T.
Science 293, 668-672, 2001
A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure, M.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
A;Reference number: A96039; MUID:21368234; PMID:11474104
A;Contents: annotation
C;Genetics:
A;Gene: SMB20676
A;Genome: plasmid

Query Match 56.6%; Score 43; DB 2; Length 306;
Best Local Similarity 57.1%; Pred. No. 9.5;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

Qy 2 KPKEAYKAAAPAA 15
Db 66 RPQPEAFESAAAPAA 79

RESULT 3
B81081
tryptophanyl-tRNA synthetase NMB1471 [imported] - Neisseria meningitidis (strain MC58 serotype 4)
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: B81081
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xu, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Venter, J.; White, O.; Salzberg, S.L.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xu, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: B81081
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-336 <TET>
A;Cross-references: UNIPROT:Q9JYQ9; GB:AE002496; GB:AE002098; NID:g7226701; PIDN:AAF4182
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB1471
C;Superfamily: tryptophan-tRNA ligase

Query Match 56.6%; Score 43; DB 2; Length 336;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15
Db 243 ESPLFEIYKAFSTPS 257

RESULT 4
E81863
tryptophan-tRNA ligase (EC 6.1.1.2) NMA1682 [imported] - Neisseria meningitidis (strain 49226)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: E81863
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel, P.; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, A.L.; White, O.; Salzberg, S.L.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; Xu, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: E81863
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-336 <PAR>
A;Cross-references: UNIPROT:Q9JYQ9; GB:AL162756; GB:AL157959; NID:g7380091; PIDN:CAB84911
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: trpS; NMA1682
C;Superfamily: tryptophan-tRNA ligase
C;Keywords: ligase

Query Match 56.6%; Score 43; DB 2; Length 336;
Best Local Similarity 53.3%; Pred. No. 10;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EKPKFEAYKAAAPAA 15
Db 243 ESPLFEIYKAFSTPS 257

RESULT 5
G87332
hypothetical protein CC0674 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: G87332
R;Niernman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.A.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolonitskii, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: A87249; MUID:21173698; PMID:11259647
A;Accession: G87332
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-389 <STO>
A;Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:g13421893; PIDN:AAK22659.1; GSPDB:G13421893
C;Genetics:
A;Gene: CC0674

Query Match 56.6%; Score 43; DB 2; Length 389;
Best Local Similarity 64.3%; Pred. No. 12;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPKEAYKAAAPAA 15
Db 66 KTSVETFKAAAPAA 79

RESULT 6
T14643
1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO1 [similarity] - sorghum
N;Alternate names: ACC oxidase
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14643
R;Finlayson, S.A.; Lee, I.J.; Mullet, J.E.; Morgan, P.W.
Plant Physiol. 119, 1083-1089, 1999
A;Title: The mechanism of rhythmic ethylene production in sorghum. The role of phytochrome in the regulation of ethylene production.
A;Reference number: Z18166; MUID:99169299; PMID:10069847
A;Accession: T14643
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-316 <FIN>
A;Cross-references: UNIPROT:O81606; EMBL:AF079588; NID:g3386564; PIDN:AAC28488.1; PID:g3386564
C;Genetics:
A;Gene: ACO1
C;Function:
A;Description: catalyzes the reaction of 1-aminocyclopropane-1-carboxylic acid, oxygen and water
A;Pathway: ethylene biosynthesis
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C;Keywords: ethylene biosynthesis; oxidoreductase

Query Match 55.9%; Score 42.5; DB 2; Length 316;
Best Local Similarity 55.6%; Pred. No. 12;

	Matches	10;	Conservative	4;	Mismatches	1;	Indels	3;	Gaps	1;
Qy	1	EXPKFEAYKAAA	---	APA	15					
		:::		:::						
Db	298	KEPRFEAYKAAAPKSSPA			315					

RESULT 7
T31225
traF protein homolog - Sphingomonas aromaticivorans plasmid pNL1
C:Species: Sphingomonas aromaticivorans
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C:Accession: T31225
R:Romine, M.F.; Stillwell, L.C.; Wong, K.K.; Thurston, S.J.; Sisk, E.C.; Sensen, C.W.; G
submitted to the EMBL Data Library, July 1998
A:Description: Complete sequence of a 184 kb catabolic plasmid from Sphingomonas aromatic
A:Reference number: Z20992
A:Accession: T31225
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: DNA
A:Residues: 1-270 <ROM>
A:Cross-references: UNIPROT:O85933; EMBL:AF079317; NID:G33378261; PID:G33378366; PIDN:AADO
C:Genetics:
A:Genome: plasmid pNL1
A:Note: traF

```
Query Match          55.3%; Score 42; DB 2; Length 270;
Best Local Similarity 76.9%; Pred. No. 12;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
```

Qy 1 EKPKEAYKAAAA 13
|||||
54 EKPKEEPKAAAA 66
Db

RESULT 8
S68365
C:(+)-delta-cadinene synthase isozyme XC1 - *Gossypium arboreum*
C:Species: *Gossypium arboreum*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68365
R:Chen, X.Y.; Chen, Y.; Heinsteins, P.; Davisson, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A:Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A:Reference number: S68365; MUID:96132653; PMID:8554317
A:Accession: S68365
A:Molecule type: mRNA
A:Residues: 1-554 <CHE>
A:Cross-references: UNIPROT:Q39761; EMBL:U23206; NID:g1045311; PIDN:AAA93064.1; PID:g104
A:Experimental source: cultivar Nanking
C:Superfamily: vetispiradiene synthase 1
C:Keywords: phytoalexin biosynthesis

Query Match 55.3%; Score 42; DB 2; Length 554;
Best Local Similarity 61.5%; Pred. NO. 25;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 2 KPKFEAYKAAAP 14
||| : |||
Db 394 KPSFEFFKANALP 406

RESULT 9
S68366
(+)-delta-cadinene synthase isozyme XC14 - *Gossypium arboreum*
C:Species: *Gossypium arboreum*
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C:Accession: S68366
R:Chen, X.Y.; Chen, Y.; Weinstein, P.; Davisson, V.J.
Arch. Biochem. Biophys. 324, 255-266, 1995
A:Title: Cloning, expression, and characterization of (+)-delta-cadinene synthase: a cat
A:Reference number: S68365; MUID:96132653; PMID:8554317
A:Accession: S68366

A:Molecule type: mRNA
A:Residues: 1-554 <CHE>
A:Cross-references: UNIPROT:Q39760; EMBL:U23205; NID:gi045313; PID:AAA93065.1; PID:gi045313.1
A:Experimental source: cultivar Nanking
C:Superfamily: vetispiradiene synthase 1
C:Keywords: phytoalexin biosynthesis

Query Match 55.3%; Score 42; DB 2; Length 554;
Best Local Similarity 61.5%; Pred. No. 25;
Matches 8; Conservative 1; Mismatches 4; Indels

QY 2 KPKFEAYKAAAAP 14
|||:|
Db 394 KPSEEFKANALP 406

RESULT 10
MOCH4E

myosin alkali light chain 4, embryonic - chicken
 N:Alternate names: myosin L23 catalytic light chain
 C:Species: Gallus gallus (chicken)
 C:Date: 01-Dec-1989 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C:Accession: S02065; A29473
 R:Nabeshima, Y.I.; Nabeshima, Y.; Kawashima, M.; Nakamura, S.; Fujii-Kuriyama, Y.
 J. Mol. Biol. 204, 497-505, 1988
 A:Title: Isolation of the chick myosin alkali light chain gene expressed in embryonic g
 A:Reference number: S02065; MUID:89141751; PMID:3225843
 A:Accession: S02065
 A:Molecule type: DNA
 A:Residues: 1-185 <NAB>
 A:Cross-references: UNIPROT:P09540; EMBL:X14428
 A:Note: the authors translated the codon CCG for residue 71 as Ala
 R:Kawashima, M.; Nabeshima, Y.; Obinata, T.; Fujii-Kuriyama, Y.

A:Title: A common myosin light chain is expressed in ch
A:Reference number: A29473; MUID:88032983; PMID:3667580
A:Accession: A29473

A;Molecule type: mRNA
A;Residues: 1-93,'L', 95-165,'L', 167-185 <KAW>
A;Cross-references: GB:J02823; NID:G212339; PIDN:AAA48957.1; PID:G212340
A;Note: the authors translated the codon CTG for residue 94 as Met and TAC for residue 95 as Tyr
C;Comment: In chicken, this form is transiently expressed in embryonic skeletal, cardiac and brain tissue
C;Genetics:
A;Introns: 33/3; 43/1; 93/1; 151/1; 177/1
A;Complex: The myosin molecule contains two heavy chains, two alkali light chains, and two essential light chains
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: brain; calcium binding; duplication; EF hand; muscle contraction
F;39-73/Domain: calmodulin repeat homology <EF1>
F;118-150/Domain: calmodulin repeat homology <EF3>
F;153-185/Domain: calmodulin repeat homology <EF4>

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Query Match      53.9%; Score 41; DB 1; Length 185;
Best Local Similarity 75.0%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 3 PKFEAYKAAAAP 14
||:|||||
pb 8 PKDDAAKAAAAP 19

RESULT 11
MORT4E

myosin alkali light chain 4, embryonic and atrial - rat
 N:Alternate names: MLC1A; MLC1emb; myosin L1 catalytic light chain, atrial
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 29-Jan-1993 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
 C:Accession: S09236
 R:Rovner, A.S.; McNally, E.M.; Leinwand, L.A.
 Nucleic Acids Res. 18, 1581-1586, 1990
 A:Title: Complete cDNA sequence of rat atrial myosin light chain 1: patterns of expression
 A:Reference number: S09236; MUID:90221887; PMID:2326197
 A:Accession: S09236
 A:Molecule type: mRNA

```

A;Residues: 1-193 <ROV>
A;Cross-references: UNIPROT:P17209; EMBL:X51531; NID:g57512; PIDN:CAA35911.1; PID:g57513
C;Comment: In mammals, this form is found in fetal and regenerating skeletal muscle, fet
C;Superfamily: calmodulin; calmodulin repeat homology
C;Keywords: calcium binding; cardiac muscle; duplication; EF hand; heart; muscle contract
F;47-81/Domain: calmodulin repeat homology <EF1>
F;126-158/Domain: calmodulin repeat homology <EF3>
F;161-193/Domain: calmodulin repeat homology <EF4>

Query Match      53.9%; Score 41; DB 1; Length 193;
Best Local Similarity 64.3%; Pred. No. 13;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 KPKEAYKAAAPA 15
   :| | | | | | |
Db 7 EPKETAKVAAAPA 20

RESULT 12
T14644
1-aminocyclopropane-1-carboxylate oxidase (EC 1.4.3.-) ACO2 - sorghum (fragment)
N;Alternate names: ACC oxidase
C;Species: Sorghum bicolor (sorghum)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T14644
R;Finlayson, S.A.; Lee, I.J.; Mullet, J.E.; Morgan, P.W.
Plant Physiol. 119, 1083-1089, 1999
A;Title: The mechanism of rhythmic ethylene production in sorghum. The role of phytochro
A;Reference number: Z18166; MUID:99169299; PMID:10069847
A;Accession: T14644
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-194 <FIN>
A;Cross-references: UNIPROT:O81607; EMBL:AF079589; NID:g3386566; PIDN:AAC28489.1; PID:g3
C;Genetics:
A;Gene: ACO2
C;Function:
A;Description: involved in ethylene biosynthesis
A;Pathway: ethylene biosynthesis
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
C;Keywords: ethylene biosynthesis; oxidoreductase

Query Match      53.9%; Score 41; DB 2; Length 194;
Best Local Similarity 53.3%; Pred. No. 13;
Matches 8; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPA 15
   ::||| | | | |
Db 180 KEPRFEAMKSAIATA 194

RESULT 13
T48130
hypothetical protein T4C9.40 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004
C;Accession: T48130
R;Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mew
submitted to the Protein Sequence Database, June 1999
A;Reference number: Z24485
A;Accession: T48130
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-200 <BEV>
A;Cross-references: UNIPROT:Q9STJ1; EMBL:AL080318
A;Experimental source: cultivar Columbia; BAC clone T4C9
C;Genetics:
A;Map position: 4
A;Introns: 132/1
A;Note: T4C9.40

Query Match      53.9%; Score 41; DB 2; Length 200;
Best Local Similarity 69.2%; Pred. No. 14;

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GN Name=RpL22; ORFNames=CG7434;
OS Drosophila melanogaster (Fruit fly);
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA Glover C.V.C., Bidwai A.P., Zhao W.F.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
RN [3]
RP GENOME REANNOTATION.
RX MEDLINE=22426069; PubMed=12537572;
RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RL Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Oregon-R;
RX MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
RA Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barrell B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,

RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourkioti F.,
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McMillan P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster.";
RL Science 287:2220-2222(2000).
CC -1- SIMILARITY: Belongs to the ribosomal protein L22e family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U42587; AAB17433.1; -;
DR EMBL; AE003418; AAF45546.1; -;
DR EMBL; AL132792; CAB60023.1; -;
DR IntAct; P50887; -;
DR FlyBase; FBgn015288; RpL22.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
DR ProDom; PD007306; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT DOMAIN 24 31 Poly-Ala.
FT DOMAIN 46 50 Poly-Ala.
FT DOMAIN 65 70 Poly-Ala.
FT DOMAIN 93 98 Poly-Ala.
FT DOMAIN 103 112 Poly-Ala.
FT DOMAIN 136 152 Poly-Ala.
FT DOMAIN 185 188 Poly-Lys.
FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).
SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;
Query Match 60.5%; Score 46; DB 1; Length 299;
Best Local Similarity 73.3%; Pred No. 17;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 EKPKFEAYKAAAPAA 15
Db 36 EKPKAEAAKPAAPAAA 50
RESULT 3
Q9UANI PRELIMINARY; PRT; 312 AA.
AC Q9UANI;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein L22 (Fragment).
GN Name=RpL22; Synonyms=rpl22;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;
RT "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal
RT proteins, L22 and L23a, with unique histone-like amino-terminal
RT extensions.";
RL Gene 226:339-345(1999).
DR EMBL; AF080131; AAD19341.1; -;
DR FlyBase; FBgn0015288; RpL22.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.

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DR GO: GO:0003735; F:Structural constituent of ribosome; IEA.
DR GO: GO:0006412; P:protein biosynthesis; IEA.
DR InterPro: IPR002671; Ribosomal L22e.
DR Pfam: PF01776; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT NON TER 1
SQ SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;

Query Match 60.5%; Score 46; DB 2; Length 312;
Best Local Similarity 73.3%; Pred. No. 17;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAP 15
    |||||
Db 49 EKPKAEAAKPAAP 63

RESULT 4
Q7SDS7
ID Q7SDS7 PRELIMINARY; PRT; 458 AA.
AC Q7SDS7;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU03083.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamvysselis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AABX01000044; EAA34940.1; -.
SQ SEQUENCE 458 AA; 49949 MW; 196D609BF9320496 CRC64;

Query Match 60.5%; Score 46; DB 2; Length 458;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAP 15
    :|||:|
Db 78 QPKPKAAKAAAP 92

RESULT 5
Q7UTK6
ID Q7UTK6 PRELIMINARY; PRT; 800 AA.
AC Q7UTK6;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=RB3828;
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OS Rhodopirellula baltica.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416; DOI=10.1073/pnas.1431443100;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heitmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
    strain 1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294139; CAD73430.1; -.
DR InterPro; IPR001345; PG/BPGM_mutase.
DR PROSITE; PS00175; PG_MUTASE; UNKNOWN_1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 800 AA; 91385 MW; C32C861687CDB466 CRC64;

Query Match 59.2%; Score 45; DB 2; Length 800;
Best Local Similarity 57.1%; Pred. No. 63;
Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 KPKFEAYKAAAP 15
    ||:|:|:|
Db 773 KPAPDAYKSIATPA 786

RESULT 6
Q69YQ8
ID Q69YQ8 PRELIMINARY; PRT; 1340 AA.
AC Q69YQ8;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp451l127 (Fragment).
GN Name=DKFZp451l127;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RG The German cDNA Consortium;
RA Koehrer K., Beyer A., Mewes H.W., Weil B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL832376; CAH10402.1; -.
KW Hypothetical protein.
FT NON TER 1340 1340
SQ SEQUENCE 1340 AA; 145772 MW; FA4635B5B5BE64394 CRC64;

Query Match 59.2%; Score 45; DB 2; Length 1340;
Best Local Similarity 64.3%; Pred. No. 1e+02;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAP 14
    |:|:|:|
Db 634 ENEFEAYSPAAP 647

RESULT 7
Q69YQ9
ID Q69YQ9 PRELIMINARY; PRT; 1614 AA.
AC Q69YQ9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein DKFZp451A076 (Fragment).
GN Name=DKFZp451A076;
OS Homo sapiens (Human).
```


OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngl1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640413; CAE41053.1; --
DR HSSP; P44681; 1JAL.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR006074; GTP1_OBG_dom.
DR InterPro; IPR006169; GTP1_OBG_sub.
DR InterPro; IPR002917; MMR_HSR1.
DR Pfam; PF01018; GTP1_OBG; 1.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PROSITE; PS00905; GTP1_OBG; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 377;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15
| | | | | : | | | | |
Db 356 EDPFRFDASRGGAAPA 370

RESULT 11
Q7W1P2 PRELIMINARY; PRT; 377 AA.
AC Q7W1P2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable GTP-binding protein.
GN OrderedLocusNames=BPP0309;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngl1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640423; CAE40050.1; --
DR HSSP; P44681; 1JAL.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR006074; GTP1_OBG_dom.
DR

DR InterPro; IPR006169; GTP1_OBG_sub.
DR InterPro; IPR002917; MMR_HSR1.
DR Pfam; PF01018; GTP1_OBG; 1.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PROSITE; PS00905; GTP1_OBG; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 377;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15
| | | | | : | | | | |
Db 356 EDPFRFDASRGGAAPA 370

RESULT 12
Q7WQL8 PRELIMINARY; PRT; 377 AA.
AC Q7WQL8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable GTP-binding protein.
GN OrderedLocusNames=BB0312;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngl1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640437; CAE30810.1; --
DR HSSP; P44681; 1JAL.
DR GO; GO:0005525; F:GTP binding; IEA.
DR InterPro; IPR006074; GTP1_OBG_dom.
DR InterPro; IPR006169; GTP1_OBG_sub.
DR InterPro; IPR002917; MMR_HSR1.
DR Pfam; PF01018; GTP1_OBG; 1.
DR Pfam; PF01926; MMR_HSR1; 1.
DR PROSITE; PS00905; GTP1_OBG; 1.
KW Complete proteome.
SQ SEQUENCE 377 AA; 40578 MW; 837173BEEA660FB1 CRC64;

Query Match 57.9%; Score 44; DB 2; Length 377;
Best Local Similarity 53.3%; Pred. No. 45;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPAA 15
| | | | | : | | | | |
Db 356 EDPFRFDASRGGAAPA 370

RESULT 13
Q92TW2 PRELIMINARY; PRT; 306 AA.
ID Q92TW2
AC Q92TW2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)

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DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein SMB20676.
GN ORFNames=SMB20676;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymB.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoelster F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894 (2001).
DR EMBL; AL591985; CAC49783.1; -.
DR PIR; G96014; G96014.
DR InterPro; IPR009273; DUF930.
DR Pfam; PF06059; DUF930; 1.
KW Complete proteome; Hypothetical protein; Plasmid.
SQ SEQUENCE 306 AA; 32638 MW; 01D9CC644001E67E CRC64;

Query Match 56.6%; Score 43; DB 2; Length 306;
Best Local Similarity 57.1%; Pred. No. 55;
Matches 8; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 KPKEAYKAAAPAA 15
Db 66 RPQPEAFESAAAPAA 79

RESULT 14
SYW_NEIMA
ID SYW_NEIMA STANDARD; PRT; 336 AA.
AC Q9JYQ0;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TrpRS).
GN Name=trps; OrderedLocusNames=NM1682;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491.";
RL Nature 404:502-506 (2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA (Trp).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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or send an email to license@isb-sib.ch).
-----
DR EMBL; AL162756; CAB84910.1; -.
DR PIR; E81863; E81863.
DR HSSP; P00953; 1MAU.
DR HAMAP; MF_00140; -.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR TIGRFAMs; TIGR00233; trps; 1.
DR PROSITE; PS00178; AA tRNA LIGASE I; FALSE NEG.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Protein biosynthesis.
FT SITE 12 20 "HIGH" region.
FT SITE 203 207 "KMSKS" region.
FT BINDING 206 206 ATP (By similarity).
SQ SEQUENCE 336 AA; 37622 MW; 3400C34F42E34536 CRC64;

Query Match 56.6%; Score 43; DB 1; Length 336;
Best Local Similarity 53.3%; Pred. No. 60;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKPKFEAYKAAAPAA 15
Db 243 ESPLFEIYKAFSTPS 257

RESULT 15
SYW_NEIMB
ID SYW_NEIMB STANDARD; PRT; 336 AA.
AC Q9JYQ9;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan--tRNA ligase)
DE (TrpRS).
GN Name=trps; OrderedLocusNames=NM1471;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Citterone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Massignani V., Pizzo M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58.";
RL Science 287:1809-1815 (2000).
CC -!- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA (Trp) = AMP +
CC diphosphate + L-tryptophanyl-tRNA (Trp).
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the class-I aminoacyl-tRNA synthetase
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
```

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; AE002496; AAF41828.1; --
DR PIR; B81081; B81081.
DR HSSP; P00953; 1MAU.
DR TIGR; NMB1471; --
DR HAMAP; MF_00140; --; 1.
DR InterPro; IPR002305; tRNA-synt_1b.
DR InterPro; IPR001412; tRNA-synt_1.
DR InterPro; IPR002306; Trp tRNA-synt_1b.
DR Pfam; PF00579; tRNA-synt_1b; 1.
DR PRINTS; PR01039; TRNASYNTHTRP.
DR PROSITE; PS00178; AA_TRNA_LIGASE_1; FALSE_NEG.
KW Aminoacyl-tRNA synthetase; ATP-binding; Complete proteome; Ligase;
KW Protein biosynthesis.
FT SITE 12 20 "HIGH" region.
FT SITE 203 207 "KMSKS" region.
FT BINDING 206 206 ATP (By similarity).
SQ SEQUENCE 336 AA; 37616 MW; 0AE32C8C00B621AA CRC64;

Query Match 56.6%; Score 43; DB 1; Length 336;
Best Local Similarity 53.3%; Pred.No. 60;
Matches 8; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 EKPKEAYKAAAPA 15
| | | | | : | :
Db 243 ESPLFEIYKAFSTPS 257

Search completed: March 31, 2005, 02:41:11
Job time : 82.5645 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:17:12 ; Search time 88.7903 Seconds
(without alignments)
65.338 Million cell updates/sec

Title: US-10-056-583A-95
Perfect score: 69
Sequence: 1 EKAKFEAFKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	69	100.0	15	5	ABP52301	Abp52301 HLA-DR2 m
2	64	92.8	17	5	ABP52302	Abp52302 HLA-DR2 m
3	63	91.3	15	5	ABP52271	Abp52271 HLA-DR2 m
4	63	91.3	15	5	ABP52298	Abp52298 HLA-DR2 m
5	63	91.3	17	5	ABP52294	Abp52294 HLA-DR2 m
6	63	91.3	17	5	ABP52296	Abp52296 HLA-DR2 m
7	63	91.3	19	5	ABP52295	Abp52295 HLA-DR2 m
8	61	88.4	17	5	ABP52303	Abp52303 HLA-DR2 m
9	57	82.6	15	5	ABP52270	Abp52270 HLA-DR2 m
10	56	81.2	15	5	ABP52297	Abp52297 HLA-DR2 m
11	53	76.8	15	5	ABP52291	Abp52291 HLA-DR2 m
12	53	76.8	15	5	ABP52263	Abp52263 HLA-DR2 m
13	52	75.4	15	5	ABP52272	Abp52272 HLA-DR2 m
14	51	73.9	15	5	ABP52259	Abp52259 HLA-DR2 m
15	51	73.9	15	5	ABP52257	Abp52257 HLA-DR2 m
16	50	72.5	15	5	ABP52300	Abp52300 HLA-DR2 m
17	50	72.5	15	5	ABP52304	Abp52304 HLA-DR2 m
18	49	71.0	15	5	ABP52299	Abp52299 HLA-DR2 m
19	48	69.6	15	5	ABP52253	Abp52253 HLA-DR2 m
20	48	69.6	15	5	ABP52251	Abp52251 HLA-DR2 m
21	48	69.6	15	5	ABP52239	Abp52239 HLA-DR2 m
22	47	68.1	15	5	ABP52290	Abp52290 HLA-DR2 m
23	47	68.1	15	5	ABP52261	Abp52261 HLA-DR2 m
24	47	68.1	15	5	ABP52244	Abp52244 HLA-DR2 m
25	47	68.1	15	5	ABP52292	Abp52292 HLA-DR2 m

26	47	68.1	15	5	ABP522269	Abp52269 HLA-DR2 m
27	47	68.1	15	5	ABP522262	Abp52262 HLA-DR2 m
28	46	66.7	15	5	ABP522264	Abp52264 HLA-DR2 m
29	46	66.7	15	5	ABP522267	Abp52267 HLA-DR2 m
30	46	66.7	15	5	ABP522236	Abp52236 HLA-DR2 m
31	44	63.8	15	5	ABP522265	Abp52265 HLA-DR2 m
32	44	63.8	15	5	ABP522277	Abp52277 HLA-DR2 m
33	44	63.8	15	5	ABP522280	Abp52280 HLA-DR2 m
34	43	62.3	15	5	ABP522254	Abp52254 HLA-DR2 m
35	43	62.3	15	5	ABP522255	Abp52255 HLA-DR2 m
36	43	62.3	15	5	ABP522240	Abp52240 HLA-DR2 m
37	43	62.3	15	5	ABP522241	Abp52241 HLA-DR2 m
38	43	62.3	15	5	ABP522248	Abp52248 HLA-DR2 m
39	43	62.3	15	5	ABP522249	Abp52249 HLA-DR2 m
40	43	62.3	15	5	ABP522305	Abp52305 HLA-DR2 m
41	43	62.3	299	4	ABB63276	Abb63276 Drosophil
42	43	62.3	299	8	ADS96704	Ads96704 Drosophil
43	42	60.9	15	3	AAy58969	Aay58969 Copeptide
44	42	60.9	15	3	AAy82058	Aay82058 MHC class
45	42	60.9	15	4	AAG63198	Aag63198 Peptide w

ALIGNMENTS

RESULT 1
ABP52301
ID ABP52301 standard; peptide; 15 AA.
XX
AC ABP52301;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:95.
XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX

OS Homo sapiens.
OS Synthetic.

XX WO200259143-A2.

XX PD 01-AUG-2002.

XX PF 24-JAN-2002; 2002WO-US002071.

XX PR 24-JAN-2001; 2001US-0263569P.

XX PA (HARD) HARVARD COLLEGE.

XX PI Strominger JL, Fridkis-Hareli M;

XX WPI; 2002-608439/65.

XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

XX PS Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 100.0%; Score 69; DB 5; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.00012;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 1 EKAKFEAFKAAAAA 15
| | | | | | | | | | | | | | | |

RESULT 2
ABP52302
ID ABP52302 standard; peptide; 17 AA.
XX
AC ABP52302;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:96.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
DR
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX

SQ Sequence 17 AA;

Query Match 92.8%; Score 64; DB 5; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.00087;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 3 EKAKFEAFKAAAAA 17
| | | | | | | | | | | | | | | |

RESULT 3
ABP52271
ID ABP52271 standard; peptide; 15 AA.
XX
AC ABP52271;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:65.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX WPI; 2002-608439/65.
DR
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
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CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 91.3%; Score 63; DB 5; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0011;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15

Db

||||:|:|:|:|:|:|

1 EKAKYEAYKAAAAA 15

RESULT 4

ABP52298

ID ABP52298 standard; peptide; 15 AA.

XX

AC

ABP52298;

DT

16-OCT-2002

(first entry)

DE

HLA-DR2

molecule binding peptide SEQ ID NO:92.

XX

KW

Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW

HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW

immune response; antiinflammatory; neuroprotective; proliferation;

KW

MHC class II protein inhibitor; demyelinating disease; inhibition;

KW

post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW

anti-tumour necrosis factor agent.

XX

OS

Homo sapiens.

OS

Synthetic.

XX

PN

WO200259143-A2.

XX

PD

01-AUG-2002.

XX

PF

24-JAN-2002; 2002WO-US002071.

XX

PR

24-JAN-2001; 2001US-0263569P.

XX

PA

(HARD) HARVARD COLLEGE.

PI

Strominger JL, Fridkis-Hareli M;

XX

WPI

2002-608439/65.

XX

PT

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS

Claim 28; Page 39; 54pp; English.

XX

CC

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX

SQ

Sequence 15 AA;

Query Match

Best Local Similarity

91.3%; Score 63; DB 5; Length 15;

Matches

13; Conservative

2; Mismatches

0; Indels

0; Gaps

0;

QY

1 EKAKFEAFKAAAAA 15

||||:|:|:|:|:|

Db

1 EKAKYEAYKAAAAA 15

||||:|:|:|:|:|

RESULT 5

ABP52294

ID ABP52294 standard; peptide; 17 AA.

XX

AC

ABP52294;

DT

16-OCT-2002

(first entry)

DE

HLA-DR2

molecule binding peptide SEQ ID NO:88.

XX

KW

Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW

HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW

immune response; antiinflammatory; neuroprotective; proliferation;

KW

MHC class II protein inhibitor; demyelinating disease; inhibition;

KW

post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW

anti-tumour necrosis factor agent.

XX

OS

Homo sapiens.

OS

Synthetic.

XX

PN

WO200259143-A2.

XX

PD

01-AUG-2002.

XX

PF

24-JAN-2002; 2002WO-US002071.

XX

PR

24-JAN-2001; 2001US-0263569P.

XX

PA

(HARD) HARVARD COLLEGE.

PI

Strominger JL, Fridkis-Hareli M;

XX

WPI

2002-608439/65.

XX

PT

New compositions comprising synthetic peptides in complex with a major histocompatibility complex class II HLA-DR2 protein, useful for treating a demyelinating disease, e.g. multiple sclerosis, or post-viral encephalomyelitis.

PS

Claim 28; Page 39; 54pp; English.

XX

CC

The present invention describes compositions (I) comprising a peptide with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine residues. The complex of the peptide with a major histocompatibility complex (MHC) class II HLA-DR2 protein is involved in modulating an immune response. (I) has antiinflammatory and neuroprotective activities, and can be used as a MHC class II protein inhibitor. The compositions comprising the peptides are useful for treating demyelinating diseases such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine demyelinating condition, and a side effect of administering an anti-tumour necrosis factor agents. The peptide further inhibits proliferation of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to ABP52305 represent peptides used in the exemplification of the present invention

XX

SQ

Sequence 17 AA;

Query Match

Best Local Similarity

91.3%; Score 63; DB 5; Length 17;

Matches

13; Conservative

2; Mismatches

0; Indels

0; Gaps

0;

QY

1 EKAKFEAFKAAAAA 15

||||:|:|:|:|:|

Db

3 EKAKYEAYKAAAAA 17

||||:|:|:|:|:|

RESULT 6

ABP52296

ID ABP52296 standard; peptide; 17 AA.

XX

AC

ABP52296;

DT

16-OCT-2002

(first entry)

DE

HLA-DR2

molecule binding peptide SEQ ID NO:90.

XX

XX

KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 24-JAN-2002; 2002WO-US002071.
PF
XX
XX 24-JAN-2001; 2001US-0263569P.
PR
XX
XX (HARD) HARVARD COLLEGE.
PA
XX
XX Strominger JL, Fridkis-Hareli M;
PI
XX
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
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CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 91.3%; Score 63; DB 5; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0013;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAAAA 15
Db 1 EKAKYEAYKAAAAA 15
|||||:|||||
RESULT 7
ABP52295
ID ABP52295 standard; peptide; 19 AA.
XX
AC ABP52295;
XX
XX 16-OCT-2002 (first entry)
DT
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:89.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX

OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
PN
XX
XX 01-AUG-2002.
PD
XX
XX 24-JAN-2002; 2002WO-US002071.
PF
XX
XX 24-JAN-2001; 2001US-0263569P.
PR
XX
XX (HARD) HARVARD COLLEGE.
PA
XX
XX Strominger JL, Fridkis-Hareli M;
PI
XX
XX WPI; 2002-608439/65.
DR
XX
XX New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
XX Claim 28; Page 39; 54pp; English.
PS
XX
XX The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 19 AA;
Query Match 91.3%; Score 63; DB 5; Length 19;
Best Local Similarity 86.7%; Pred. No. 0.0014;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAAAA 15
Db 3 EKAKYEAYKAAAAA 17
|||||:|||||
RESULT 8
ABP52303
ID ABP52303 standard; peptide; 17 AA.
XX
AC ABP52303;
XX
XX 16-OCT-2002 (first entry)
DT
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:97.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
XX WO200259143-A2.
PN
XX
XX 01-AUG-2002.
PD
XX

PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PS New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
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CC immune response. (I) has antiinflammatory and neuroprotective activities,
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CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 17 AA;
Query Match 88.4%; Score 61; DB 5; Length 17;
Best Local Similarity 86.7%; Pred No. 0.0027;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAATAA 15
Db 3 EKAKFEAYKAAATAA 17
RESULT 9
ABP52270
ID ABP52270 standard; peptide; 15 AA.
XX
AC ABP52270;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:64.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PS New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Claim 28; Page 39; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
CC and can be used as a MHC class II protein inhibitor. The compositions
CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;
Query Match 82.6%; Score 57; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.011;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 EKAKFEAFKAAATAA 15
Db 1 EAAKYEAYKAAATAA 15
RESULT 10
ABP52297
ID ABP52297 standard; peptide; 15 AA.
XX
AC ABP52297;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:91.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PS New compositions comprising synthetic peptides in complex with a major
XX histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.

Thu Mar 31 14:05:35 2005

XX Claim 28; Page 39; 54pp; English.

XX The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

SQ Query Match 81.2%; Score 56; DB 5; Length 15;

Best Local Similarity 80.0%; Pred. No. 0.016;

Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15

Db 1 EKPKFEAYKAAAAA 15

RESULT 11

ABP52291

ID ABP52291 standard; peptide; 15 AA.

XX

AC ABP52291;

XX

DT 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:85.

XX

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Claim 28; Page 39; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

CC ABP52305 represent peptides used in the exemplification of the present

CC invention

XX Sequence 15 AA;

SQ Query Match 76.8%; Score 53; DB 5; Length 15;

Best Local Similarity 73.3%; Pred. No. 0.049;

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15

Db 1 EKPKFEAYKAAAAA 15

RESULT 12

ABP52263

ID ABP52263 standard; peptide; 15 AA.

XX

AC ABP52263;

XX

DT 16-OCT-2002 (first entry)

XX

DE HLA-DR2 molecule binding peptide SEQ ID NO:57.

XX

XX Human leukocyte antigen; HLA; major histocompatibility complex; MHC;

KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;

KW immune response; antiinflammatory; neuroprotective; proliferation;

KW MHC class II protein inhibitor; demyelinating disease; inhibition;

KW post-viral encephalomyelitis; post-vaccine demyelinating condition;

KW anti-tumour necrosis factor agent.

XX

OS Homo sapiens.

OS Synthetic.

XX

PN WO200259143-A2.

XX

PD 01-AUG-2002.

XX

PF 24-JAN-2002; 2002WO-US002071.

XX

PR 24-JAN-2001; 2001US-0263569P.

XX

PA (HARD) HARVARD COLLEGE.

XX

PI Strominger JL, Fridkis-Hareli M;

XX

DR WPI; 2002-608439/65.

XX

XX New compositions comprising synthetic peptides in complex with a major

PT histocompatibility complex class II HLA-DR2 protein, useful for treating a

PT demyelinating disease, e.g. multiple sclerosis, or post-viral

PT encephalomyelitis.

XX

PS Example 1; Page 33; 54pp; English.

XX

CC The present invention describes compositions (I) comprising a peptide

CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine

CC residues. The complex of the peptide with a major histocompatibility

CC complex (MHC) class II HLA-DR2 protein is involved in modulating an

CC immune response. (I) has antiinflammatory and neuroprotective activities,

CC and can be used as a MHC class II protein inhibitor. The compositions

CC comprising the peptides are useful for treating demyelinating diseases

CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine

CC demyelinating condition, and a side effect of administering an anti-

CC tumour necrosis factor agents. The peptide further inhibits proliferation

CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to

RESULT 15
ABP52257
ID ABP52257 standard; peptide; 15 AA.
XX
AC ABP52257;
XX
DT 16-OCT-2002 (first entry)
XX
DE HLA-DR2 molecule binding peptide SEQ ID NO:51.
XX
KW Human leukocyte antigen; HLA; major histocompatibility complex; MHC;
KW HLA-DR2; MHC class II DR-2 molecule; demyelinating; multiple sclerosis;
KW immune response; antiinflammatory; neuroprotective; proliferation;
KW MHC class II protein inhibitor; demyelinating disease; inhibition;
KW post-viral encephalomyelitis; post-vaccine demyelinating condition;
KW anti-tumour necrosis factor agent.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200259143-A2.
XX
PD 01-AUG-2002.
XX
PF 24-JAN-2002; 2002WO-US002071.
XX
PR 24-JAN-2001; 2001US-0263569P.
XX
PA (HARD) HARVARD COLLEGE.
XX
PI Strominger JL, Fridkis-Hareli M;
XX
DR WPI; 2002-608439/65.
XX
PT New compositions comprising synthetic peptides in complex with a major
PT histocompatibility complex class II HLA-DR2 protein, useful for treating a
PT demyelinating disease, e.g. multiple sclerosis, or post-viral
PT encephalomyelitis.
XX
PS Example 1; Page 32; 54pp; English.
XX
CC The present invention describes compositions (I) comprising a peptide
CC with an amino acid sequence with tyrosine (Y), lysine (K), and/or valine
CC residues. The complex of the peptide with a major histocompatibility
CC complex (MHC) class II HLA-DR2 protein is involved in modulating an
CC immune response. (I) has antiinflammatory and neuroprotective activities,
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CC comprising the peptides are useful for treating demyelinating diseases
CC such as multiple sclerosis, post-viral encephalomyelitis, a post-vaccine
CC demyelinating condition, and a side effect of administering an anti-
CC tumour necrosis factor agents. The peptide further inhibits proliferation
CC of autoantigen-specific HLA-DR2-restricted T cell clones. ABP52207 to
CC ABP52305 represent peptides used in the exemplification of the present
CC invention
XX
SQ Sequence 15 AA;

Query Match 73.9%; Score 51; DB 5; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.11;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
| | | | |
Db 1 EAAKYAAYKAAAAA 15

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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:53 ; Search time 22.9839 Seconds
(without alignments)
48.718 Million cell updates/sec

Title: US-10-056-583A-95
Perfect score: 69
Sequence: 1 EKAKFEAFKAAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	40	58.0	1001	4 US-09-248-796A-18658	Sequence 18658, A
2	39	56.5	166	4 US-09-252-991A-22139	Sequence 22139, A
3	39	56.5	466	4 US-09-489-039A-13950	Sequence 13950, A
4	38	55.1	13	5 PCT-US95-04121-38	Sequence 38, Appl
5	38	55.1	497	1 US-08-295-670-6	Sequence 6, Appl
6	38	55.1	497	1 US-08-633-485-6	Sequence 6, Appl
7	38	55.1	510	3 US-08-508-761B-4	Sequence 4, Appl
8	37	53.6	38	3 US-09-117-121-16	Sequence 16, Appl
9	37	53.6	38	3 US-09-117-121-24	Sequence 24, Appl
10	37	53.6	38	4 US-09-344-529-5	Sequence 5, Appl
11	37	53.6	69	4 US-09-248-796A-25516	Sequence 25516, A
12	37	53.6	476	4 US-09-198-452A-1021	Sequence 1021, Ap
13	37	53.6	479	4 US-09-438-185A-950	Sequence 950, App
14	37	53.6	576	4 US-09-543-681A-7747	Sequence 7747, Ap
15	37	53.6	759	4 US-09-328-352-4241	Sequence 4241, Ap
16	36	52.2	13	5 PCT-US94-10257A-33	Sequence 33, Appl
17	36	52.2	54	3 US-09-117-121-30	Sequence 30, Appl
18	36	52.2	162	4 US-09-732-210-1445	Sequence 1445, Ap
19	36	52.2	180	6 5273901-7	Patent No. 5273901
20	36	52.2	180	6 5482709-6	Patent No. 5482709
21	36	52.2	180	6 5273901-7	Patent No. 5273901
22	36	52.2	180	6 5482709-6	Patent No. 5482709
23	36	52.2	405	4 US-09-328-352-4239	Sequence 4239, Ap
24	36	52.2	582	4 US-09-919-497-100	Sequence 100, App
25	35	50.7	10	4 US-09-060-450-5	Sequence 5, Appl
26	35	50.7	109	4 US-09-405-743A-7	Sequence 7, Appl
27	35	50.7	109	4 US-09-816-989A-7	Sequence 7, Appl

28	35	50.7	143	4 US-09-513-999C-5527	Sequence 5527, Ap
29	35	50.7	171	4 US-09-902-540-11599	Sequence 11599, A
30	35	50.7	219	4 US-09-902-540-16623	Sequence 16623, A
31	35	50.7	249	4 US-09-134-000C-3759	Sequence 3759, Ap
32	35	50.7	388	1 US-07-637-870-4	Sequence 4, Appli
33	35	50.7	388	1 US-07-637-399-7	Sequence 7, Appli
34	35	50.7	388	1 US-07-640-476-7	Sequence 7, Appli
35	35	50.7	388	1 US-08-112-703-7	Sequence 7, Appli
36	35	50.7	409	4 US-09-252-991A-26859	Sequence 26859, A
37	35	50.7	454	3 US-09-134-078-20	Sequence 20, Appl
38	35	50.7	457	4 US-09-949-016-7165	Sequence 7165, Ap
39	35	50.7	474	4 US-09-543-681A-6873	Sequence 6873, Ap
40	35	50.7	607	4 US-09-489-039A-8171	Sequence 8171, Ap
41	35	50.7	637	4 US-09-673-198-26	Sequence 26, Appl
42	35	50.7	1156	4 US-09-198-452A-171	Sequence 171, App
43	35	50.7	1562	4 US-09-438-185A-152	Sequence 152, App
44	35	50.7	1601	4 US-09-345-473E-40	Sequence 40, Appl
45	34.5	50.0	214	3 US-09-411-578-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-09-248-796A-18658
; Sequence 18658, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 18658
; LENGTH: 1001
; TYPE: PRT
; ORGANISM: Candida albicans
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (21)
; OTHER INFORMATION: Identity of amino acid sequences at the above locations are unknown
US-09-248-796A-18658

Query Match 58.0%; Score 40; DB 4; Length 1001;
Best Local Similarity 78.6%; Pred. No. 1.6e+02;
Matches 11; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 KAKFEAFKAAAAAA 15
||| || |||||
Db 818 KAKEAEAEAAAAAA 831

RESULT 2
US-09-252-991A-22139
; Sequence 22139, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27

; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22139
; LENGTH: 166
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22139

Query Match 56.5%; Score 39; DB 4; Length 166;
Best Local Similarity 64.3%; Pred. No. 39;
Matches 9; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 KAKFEAFKAAAAAA 15
|:|:|:|:|:|:|
Db 104 KAQVDAFHAAALAA 117

RESULT 3
US-09-489-039A-13950
; Sequence 13950, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 13950
; LENGTH: 466
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-13950

Query Match 56.5%; Score 39; DB 4; Length 466;
Best Local Similarity 76.9%; Pred. No. 1.1e+02;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 AKFEAFKAAAAAA 15
|:|:|:|:|:|:|
Db 153 ASLEAQKAAAAAA 165

RESULT 4
PCT-US95-04121-38
; Sequence 38, Application PC/TUS9504121
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Haptenated Peptides and Uses Thereof
; NUMBER OF SEQUENCES: 62
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04121
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/222,206
; FILING DATE: April 1, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Vanstone, Darlene A.
; REGISTRATION NUMBER: 35,279
; REFERENCE/DOCKET NUMBER: 079.2PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6010
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
PCT-US95-04121-38

Query Match 55.1%; Score 38; DB 5; Length 13;
Best Local Similarity 69.2%; Pred. No. 4.6;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AKFEAFKAAAAAA 15
|:|:|:|:|:|:|
Db 1 AAYKAAKAAAAAA 13

RESULT 5
US-08-295-670-6
; Sequence 6, Application US/08295670
; Patent No. 5547864
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, HISASHI
; APPLICANT: TSUCHIYA, MAKOTO
; APPLICANT: MIWA, KIYOSHI
; APPLICANT: KAWAHARA, YOSHIO
; TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/295,670
; FILING DATE: 08-SEP-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP94/00039
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-4069
; FILING DATE: 13-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5547864man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-697-0 PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-295-670-6

Query Match 55.1%; Score 38; DB 1; Length 497;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAAA 15
|:|:|:|:|:|:|

Db 104 EQAAFEAFEAARVRA 118

RESULT 6

US-08-633-485-6
; Sequence 6, Application US/08633485
; Patent No. 5681717
; GENERAL INFORMATION:
; APPLICANT: KAWASAKI, HISASHI
; APPLICANT: TSUCHIYA, MAKOTO
; APPLICANT: MIWA, KIYOSHI
; APPLICANT: KAWAHARA, YOSHIO
; TITLE OF INVENTION: THE NOVEL CELL SURFACE PROTEIN
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
; ADDRESSEE: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/633,485
; FILING DATE: 17-APR-1996
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/295,670
; FILING DATE: 08-SEP-1994
; APPLICATION NUMBER: PCT/JP94/00039
; FILING DATE: 13-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 5-4069
; FILING DATE: 13-JAN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5681717man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 10-697-0 PCT

; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248855 OPAT UR
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 497 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-633-485-6

Query Match 55.1%; Score 38; DB 1; Length 497;
Best Local Similarity 53.3%; Pred. No. 1.6e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|:|:|:|:|:|:|
Db 104 EQAAFEAFEAARVRA 118

RESULT 7

US-08-508-761B-4
; Sequence 4, Application US/08508761B
; Patent No. 6027920
; GENERAL INFORMATION:
; APPLICANT: Joliff, Gwennael
; APPLICANT: Guyonvarch, Armel
; APPLICANT: Purification, Relano
; APPLICANT: Duchiron, Francis

; APPLICANT: Renaud, Michel
; TITLE OF INVENTION: System for Protein Expression and
; SECRETION ESPECIALLY IN CORYNEBACTERIA
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jacobson, Price, Holman & Stern, PLLC
; STREET: 400 Seventh St. N.W.
; CITY: Washington D.C.
; COUNTRY: U.S.A.
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/508,761B
; FILING DATE: 31-JUL-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09652
; FILING DATE: 29-JUL-1991

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91/09870
; FILING DATE: 02-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Player, William E.
; REGISTRATION NUMBER: 31,409
; REFERENCE/DOCKET NUMBER: P58525NA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-6666
; TELEFAX: (202) 393-5350

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 510 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-508-761B-4

Query Match 55.1%; Score 38; DB 3; Length 510;
Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|:|:|:|:|:|:|
Db 104 EQAAFEAFEAARVRA 118

RESULT 8

US-09-117-121-16
; Sequence 16, Application US/09117121
; Patent No. 6307020
; GENERAL INFORMATION:

; APPLICANT: Hew, Choy
; APPLICANT: Gong, Zhiyuan
; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
; TITLE OF INVENTION: and Nucleic Acids
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/117,121
; FILING DATE: 20-NOV-1998

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; CLASSIFICATION: 435
; PRIOR APPLICATION DATA: WO PCT/CA97/00062
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 016252-001610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-117-121-16

Query Match 53.6%; Score 37; DB 3; Length 38;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
Db 16 KAAAEATKAAAAKA 29

RESULT 9
US-09-117-121-24
; Sequence 24, Application US/09117121
; Patent No. 6307020
; GENERAL INFORMATION:
; APPLICANT: Hew, Choy
; APPLICANT: Gong, Zhiyuan
; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
; TITLE OF INVENTION: Intracellular Antifreeze Polypeptides
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/117,121
; FILING DATE: 20-NOV-1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA97/00062
; FILING DATE: 30-JAN-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 016252-001610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-117-121-24

Query Match 53.6%; Score 37; DB 3; Length 38;

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Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
Db 16 KAAAEATKAAAAKA 29

RESULT 10
US-09-344-529-5
; Sequence 5, Application US/09344529
; Patent No. 6429293
; GENERAL INFORMATION:
; APPLICANT: Hew, Choy L.
; APPLICANT: HSC Research and Development Limited Partnership
; TITLE OF INVENTION: Sculptin-Type Antifreeze Polypeptides and Nucleic Acids
; FILE REFERENCE: 016252-002620US
; CURRENT APPLICATION NUMBER: US/09/344,529
; CURRENT FILING DATE: 1999-06-24
; EARLIER APPLICATION NUMBER: US 60/090,794
; EARLIER FILING DATE: 1998-06-26
; EARLIER APPLICATION NUMBER: US 60/095,713
; EARLIER FILING DATE: 1998-08-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Pleuronectes americanus
; FEATURE:
; OTHER INFORMATION: Winter flounder skin-type antifreeze polypeptide
US-09-344-529-5

Query Match 53.6%; Score 37; DB 4; Length 38;
Best Local Similarity 71.4%; Pred. No. 19;
Matches 10; Conservative 0; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
Db 16 KAAAEATKAAAAKA 29

RESULT 11
US-09-248-796A-25516
; Sequence 25516, Application US/09248796A
; Patent No. 6747137
; GENERAL INFORMATION:
; APPLICANT: Keith Weinstock et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.132
; CURRENT APPLICATION NUMBER: US/09/248,796A
; CURRENT FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,725
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/096,409
; PRIOR FILING DATE: 1998-08-13
; NUMBER OF SEQ ID NOS: 28208
; SEQ ID NO 25516
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Candida albicans
US-09-248-796A-25516

Query Match 53.6%; Score 37; DB 4; Length 69;
Best Local Similarity 57.1%; Pred. No. 34;
Matches 8; Conservative 2; Mismatches 4; Indels 4; Gaps 0;

QY 2 KAKFEAFKAAAAA 15
Db 8 EAKLDTFPAATAA 21

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RESULT 12
US-09-198-452A-1021
; Sequence 1021, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1021
; LENGTH: 476
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-1021

Query Match      53.6%; Score 37; DB 4; Length 476;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 KFEAFKAAAA 14
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Db      107 RFSAFAAAAA 117

RESULT 13
US-09-438-185A-950
; Sequence 950, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia Pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1998-11-12
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 950
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPn0948
US-09-438-185A-950

Query Match      53.6%; Score 37; DB 4; Length 479;
Best Local Similarity 72.7%; Pred. No. 2.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      4 KFEAFKAAAA 14
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Db      110 RFSAFAAAAA 120

RESULT 14
US-09-543-681A-7747
; Sequence 7747, Application US/09543681A
; Patent No. 6505709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
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; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 7747
; LENGTH: 576
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-7747

Query Match      53.6%; Score 37; DB 4; Length 576;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      1 EKAKFEAFKAAAA 14
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Db      311 EEEQFQAYKAVAEA 324

RESULT 15
US-09-328-352-4241
; Sequence 4241, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 4241
; LENGTH: 759
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-4241

Query Match      53.6%; Score 37; DB 4; Length 759;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 10; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      2 KAKFEAFKAAAA 15
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Db      444 KAKEEQAKAAAKAA 457

Search completed: March 31, 2005, 02:44:10
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 02:29:23 ; Search time 66.5323 Seconds
(without alignments)
74.648 Million cell updates/sec

Title: US-10-056-583A-95
Perfect score: 69
Sequence: 1 EKAKFEAFKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1407402 seqs, 331100923 residues

Total number of hits satisfying chosen parameters: 1407402

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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2	64	92.8	17	14	US-10-056-583-96	Sequence 96, Appl
3	63	91.3	15	14	US-10-056-583-65	Sequence 65, Appl
4	63	91.3	17	14	US-10-056-583-88	Sequence 88, Appl
5	63	91.3	17	14	US-10-056-583-90	Sequence 90, Appl
6	63	91.3	19	14	US-10-056-583-89	Sequence 89, Appl
7	61	88.4	17	14	US-10-056-583-97	Sequence 97, Appl
8	57	82.6	15	14	US-10-056-583-64	Sequence 64, Appl
9	57	82.6	15	14	US-10-056-583-92	Sequence 92, Appl
10	56	81.2	15	14	US-10-056-583-91	Sequence 91, Appl
11	53	76.8	15	14	US-10-056-583-57	Sequence 57, Appl
12	53	76.8	15	14	US-10-056-583-85	Sequence 85, Appl
13	52	75.4	15	14	US-10-056-583-66	Sequence 66, Appl

14	51	73.9	15	14	US-10-056-583-51	Sequence 51, Appl
15	51	73.9	15	14	US-10-056-583-53	Sequence 53, Appl
16	50	72.5	15	14	US-10-056-583-94	Sequence 94, Appl
17	50	72.5	15	14	US-10-056-583-98	Sequence 98, Appl
18	49	71.0	15	14	US-10-056-583-93	Sequence 93, Appl
19	48	69.6	15	14	US-10-056-583-33	Sequence 33, Appl
20	48	69.6	15	14	US-10-056-583-45	Sequence 45, Appl
21	48	69.6	15	14	US-10-056-583-47	Sequence 47, Appl
22	47	68.1	15	14	US-10-056-583-38	Sequence 38, Appl
23	47	68.1	15	14	US-10-056-583-55	Sequence 55, Appl
24	47	68.1	15	14	US-10-056-583-56	Sequence 56, Appl
25	47	68.1	15	14	US-10-056-583-63	Sequence 63, Appl
26	47	68.1	15	14	US-10-056-583-84	Sequence 84, Appl
27	47	68.1	15	14	US-10-056-583-86	Sequence 86, Appl
28	46	66.7	15	14	US-10-056-583-30	Sequence 30, Appl
29	46	66.7	15	14	US-10-056-583-58	Sequence 58, Appl
30	46	66.7	15	14	US-10-056-583-61	Sequence 61, Appl
31	44	63.8	15	14	US-10-056-583-59	Sequence 59, Appl
32	44	63.8	15	14	US-10-056-583-71	Sequence 71, Appl
33	44	63.8	15	14	US-10-056-583-74	Sequence 74, Appl
34	43	62.3	15	14	US-10-056-583-34	Sequence 34, Appl
35	43	62.3	15	14	US-10-056-583-35	Sequence 35, Appl
36	43	62.3	15	14	US-10-056-583-42	Sequence 42, Appl
37	43	62.3	15	14	US-10-056-583-43	Sequence 43, Appl
38	43	62.3	15	14	US-10-056-583-48	Sequence 48, Appl
39	43	62.3	15	14	US-10-056-583-49	Sequence 49, Appl
40	43	62.3	15	14	US-10-056-583-99	Sequence 99, Appl
41	43	62.3	99	16	US-10-437-963-141270	Sequence 141270,
42	43	62.3	142	16	US-10-437-963-141271	Sequence 141271,
43	42	60.9	15	9	US-09-765-301-24	Sequence 24, Appl
44	42	60.9	15	10	US-09-765-644A-24	Sequence 24, Appl
45	42	60.9	15	14	US-10-056-583-25	Sequence 25, Appl

ALIGNMENTS

RESULT 1
US-10-056-583-95
; Sequence 95, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 95
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-95

Query Match 100.0%; Score 69; DB 14; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.5e-05;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 EKAKFEAFKAAAAA 15

RESULT 2
US-10-056-583-96

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; Sequence 96, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 96
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-96
```

```
Query Match      92.8%; Score 64; DB 14; Length 17;
Best Local Similarity 93.3%; Pred. No. 0.00043;
Matches 14; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db       3 EKAKFEAFKAAAPA 17
```

```
RESULT 3
US-10-056-583-65
; Sequence 65, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 65
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-65
```

```
Query Match      91.3%; Score 63; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.00055;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db       1 EKAKYEAYKAAAAA 15
```

```
RESULT 4
US-10-056-583-88
; Sequence 88, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
```

```
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 88
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-88
```

```
Query Match      91.3%; Score 63; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.00063;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db       3 EKAKYEAYKAAAAA 17
```

```
RESULT 5
US-10-056-583-90
; Sequence 90, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 90
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-90
```

```
Query Match      91.3%; Score 63; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.00063;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db       1 EKAKYEAYKAAAAA 15
```

```
RESULT 6
US-10-056-583-89
; Sequence 89, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
```



```

; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-89

```

```

Query Match      91.3%; Score 63; DB 14; Length 19;
Best Local Similarity 86.7%; Pred. No. 0.00071;
Matches 13; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db      3 EKAKYEAYKAAAAA 17

```

```

RESULT 7
US-10-056-583-97
; Sequence 97, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-97

```

```

Query Match      88.4%; Score 61; DB 14; Length 17;
Best Local Similarity 86.7%; Pred. No. 0.0014;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db      3 EKAKFEAYKAAAAA 17

```

```

RESULT 8
US-10-056-583-64
; Sequence 64, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0

```

```

; SEQ ID NO 64
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-64

```

```

Query Match      82.6%; Score 57; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0056;
Matches 12; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db      1 EAAKYEAYKAAAAA 15

```

```

RESULT 9
US-10-056-583-92
; Sequence 92, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-92

```

```

Query Match      82.6%; Score 57; DB 14; Length 15;
Best Local Similarity 86.7%; Pred. No. 0.0056;
Matches 13; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      1 EKAKFEAFKAAAAA 15
        |||||:|||||
Db      1 EAAKYEAYKAAAAA 15

```

```

RESULT 10
US-10-056-583-91
; Sequence 91, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 91
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

```

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-91

Query Match 81.2%; Score 56; DB 14; Length 15;
Best Local Similarity 80.0%; Pred. No. 0.0082;
Matches 12; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|||:|||||
Db 1 EKPKEAYKAAAAA 15

RESULT 11

US-10-056-583-57
; Sequence 57, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 57
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-57

Query Match 76.8%; Score 53; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.026;
Matches 11; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|||:|||||
Db 1 EAKYAYKAAAAA 15

RESULT 12

US-10-056-583-85
; Sequence 85, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 85
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-85

Query Match 76.8%; Score 53; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.026;

Qy 1 EKAKFEAFKAAAAA 15
|||:|||||
Db 1 EAKYAYKAAAAA 15

Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|||:|||||
Db 1 EKPKEAYKAAAAA 15

RESULT 13

US-10-056-583-66
; Sequence 66, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 66
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-66

Query Match 75.4%; Score 52; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.038;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|||:|||||
Db 1 EAKYAYKAAAAA 15

RESULT 14

US-10-056-583-51
; Sequence 51, Application US/10056583
; Publication No. US20030064915A1
; GENERAL INFORMATION:
; APPLICANT: Presidents and Fellows of Harvard College
; APPLICANT: Strominger, Jack L.
; APPLICANT: Fridkis-Hareli, Masha
; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 24655-017
; CURRENT APPLICATION NUMBER: US/10/056,583
; CURRENT FILING DATE: 2002-01-24
; PRIOR APPLICATION NUMBER: 60/263,569
; PRIOR FILING DATE: 2001-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: The peptide was designed and synthesized.
US-10-056-583-51

Query Match 73.9%; Score 51; DB 14; Length 15;
Best Local Similarity 73.3%; Pred. No. 0.056;
Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
|||:|||||
Db 1 EAKYAYKAAAAA 15

RESULT 15
 US-10-056-583-53
 ; Sequence 53, Application US/10056583
 ; Publication NO. US20030064915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Presidents and Fellows of Harvard College
 ; APPLICANT: Strominger, Jack L.
 ; APPLICANT: Fridkis-Hareli, Masha
 ; TITLE OF INVENTION: THERAPEUTIC PEPTIDES FOR DEMYELINATING
 ; TITLE OF INVENTION: CONDITIONS
 ; FILE REFERENCE: 24655-017
 ; CURRENT APPLICATION NUMBER: US/10/056,583
 ; CURRENT FILING DATE: 2002-01-24
 ; PRIOR APPLICATION NUMBER: 60/263,569
 ; PRIOR FILING DATE: 2001-01-24
 ; NUMBER OF SEQ ID NOS: 99
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 53
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: The peptide was designed and synthesized.
 US-10-056-583-53

Query Match 73.9%; Score 51; DB 14; Length 15;
 Best Local Similarity 73.3%; Pred. No. 0.056;
 Matches 11; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 EKAKFEAFKAAAAA 15
 ||| : |||||
 Db 1 EKAAYAAYKAAAAA 15

Search completed: March 31, 2005, 02:48:49
 Job time : 67.5323 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:26:17 ; Search time 17.9032 Seconds
(without alignments)
80.614 Million cell updates/sec

Title: US-10-056-583A-95
Perfect score: 69
Sequence: 1 EKAKFEAFKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			DB ID	Description
	Score	Match	Length		
1	47.5	68.8	189	2 S77930	exoskeletal protei
2	47.5	68.8	189	2 S77935	exoskeletal protei
3	42	60.9	179	2 F97683	50S ribosomal prot
4	42	60.9	179	2 AF2908	50S ribosomal prot
5	41	59.4	346	2 C82156	conserved hypothet
6	41	59.4	828	2 F96535	hypothetical prote
7	40	58.0	478	2 S04675	H+-transporting tw
8	40	58.0	698	2 T32594	hypothetical prote
9	39	56.5	73	2 S40015	phd protein - phag
10	39	56.5	113	2 T30041	hypothetical prote
11	39	56.5	144	2 D83152	hypothetical prote
12	39	56.5	198	2 AI2622	conserved hypothet
13	39	56.5	217	2 A97405	hypothetical prote
14	39	56.5	250	2 T51971	proteasome endopep
15	39	56.5	389	2 G87332	hypothetical prote
16	39	56.5	421	2 JV0057	tola protein - Esc
17	39	56.5	2957	2 T33152	hypothetical prote
18	38	55.1	151	1 GGICEH	globin CTT-VIII -
19	38	55.1	246	2 B72728	probable ribosomal
20	38	55.1	320	2 S76422	hypothetical prote
21	38	55.1	436	2 T31902	hypothetical prote
22	38	55.1	510	2 S35028	protein PS2 precur
23	38	55.1	525	1 QQBE6	BFLF1 protein - hu
24	37	53.6	231	2 T02585	hypothetical prote
25	37	53.6	254	2 H86355	probable 14-3-3 pr
26	37	53.6	270	2 G82108	conserved hypothet
27	37	53.6	359	2 H95865	probable fructose-
28	37	53.6	476	2 C72016	glycogen synthase
29	37	53.6	476	2 B86609	glycogen synthase

30	37	53.6	575	2 AC0364	phosphoenolpyruvat
31	37	53.6	795	2 F75154	cell division cont
32	37	53.6	829	2 E64114	translation initia
33	37	53.6	840	2 D75046	translational endop
34	37	53.6	1430	2 T34516	hypothetical prote
35	37	53.6	1465	2 S43529	165K protein, skel
36	36	52.2	162	2 H70927	probable rpsp prot
37	36	52.2	165	2 B87702	ribosomal protein
38	36	52.2	206	2 S43445	translation elonga
39	36	52.2	251	2 C70521	1-acylglycerol-3-p
40	36	52.2	273	2 T51010	hypothetical prote
41	36	52.2	287	2 T51011	hypothetical prote
42	36	52.2	305	1 R5DOP0	ribosomal protein
43	36	52.2	306	2 C70410	hypothetical prote
44	36	52.2	320	2 B86255	hypothetical prote
45	36	52.2	321	2 A44230	phthalate dioxygen

ALIGNMENTS

RESULT 1

S77930
exoskeletal protein HACP202A - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77930
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homarus americanus
A;Reference number: S77925
A;Accession: S77930
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M496

Query Match 68.8%; Score 47.5; DB 2; Length 189;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 EKAK-FEAFKAAAAA 15

DB 11 EKARFFQAFKAAEAAA 26

RESULT 2

S77935
exoskeletal protein HACP202B - American lobster (fragment)
C;Species: Homarus americanus (American lobster)
C;Date: 23-Jul-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C;Accession: S77935
R;Nousiainen, M.; Rafn, K.; Skou, L.; Roepstorff, P.; Andersen, S.O.
submitted to the Protein Sequence Database, June 1997
A;Description: Characterization of exoskeletal proteins from the American lobster, Homarus americanus
A;Reference number: S77925
A;Accession: S77935
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-189 <NOU>
A;Cross-references: UNIPROT:Q7M495

Query Match 68.8%; Score 47.5; DB 2; Length 189;
Best Local Similarity 75.0%; Pred. No. 1.3;
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 EKAK-FEAFKAAAAA 15

DB 11 EKARFFQAFKAAEAAA 26

RESULT 3

F97683

50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Cereon)
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: F97683
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughy, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97683
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE007869; PIDN:AAK88423.1; PID:gl15157917; GSPDB:C
C;Genetics:
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match 60.9%; Score 42; DB 2; Length 179;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 137 EKARLEAEKVAAAAQA 151
|||: ||| ||| |

RESULT 4
AF2908
50S ribosomal protein L19 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AF2908
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, D.; erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClellan; Karp, P.; Romero, P.; Zhang, S. Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AF2908
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-179 <KUR>
A;Cross-references: UNIPROT:Q8UBZ5; GB:AE008688; PIDN:AAL43684.1; PID:gl17741210; GSPDB:C
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: rplS
A;Map position: circular chromosome
C;Superfamily: Escherichia coli ribosomal protein L19

Query Match 60.9%; Score 42; DB 2; Length 179;
Best Local Similarity 66.7%; Pred. No. 9.5;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 137 EKARLEAEKVAAAAQA 151
|||: ||| ||| |

RESULT 5
C82156
conserved hypothetical protein VC1791 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: C82156
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F. Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82156
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-346 <HEI>
A;Cross-references: UNIPROT:Q9KR55; GB:AE004256; GB:AE003852; NID:g9656310; PIDN:AAF9494
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC1791
A;Map position: 1

Query Match 59.4%; Score 41; DB 2; Length 346;
Best Local Similarity 90.0%; Pred. No. 25;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 EAFKAAAAAA 15
Db 307 EAFKSAAAAA 316
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RESULT 6
F96535
hypothetical protein F10F5.13 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: F96535
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federaspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.-A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I. ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: F96535
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-828 <STO>
A;Cross-references: UNIPROT:Q9C6C7; GB:AE005173; NID:gl0092168; PIDN:AAG12588.1; GSPDB:GN
C;Genetics:
A;Gene: F10F5.13
A;Map position: 1

Query Match 59.4%; Score 41; DB 2; Length 828;
Best Local Similarity 69.2%; Pred. No. 56;
Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAA 13
Db 158 EKAAVEAFEAASA 170
|||: ||| ||| |

RESULT 7
S04675
H+-transporting two-sector ATPase (EC 3.6.3.14) beta chain - Rhodopseudomonas blastica
C;Species: Rhodopseudomonas blastica
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C;Accession: S04675
R;Tybulewicz, V.L.J.; Falk, G.; Walker, J.E. J. Mol. Biol. 179, 185-214, 1984
A;Title: Rhodopseudomonas blastica atp operon. Nucleotide sequence and transcription.
A;Reference number: S04666; MUID:85058188; PMID:6209404
A;Accession: S04675
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-478 <TYB>
A;Cross-references: UNIPROT:P05440
C;Superfamily: H+-transporting ATP synthase alpha chain; H+-transporting ATP synthase alpha C;Keywords: ATP biosynthesis; hydrolase; membrane-associated complex; nucleotide binding; F;155-162/Region: nucleotide-binding motif A (P-loop)

```
Qy      2 KAKFEAFKAAAAA 15
         |||||:||||
Db     41 KATFEAYKKAALDA 54
```

• •

A; Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AI2622
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-198 <KUR>
A;Cross-references: UNIPROT:Q8UIC0; GB:AE008688; PIDN:AAL41399.1; PID:gl7738717; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: Atu0377
A;Map position: circular chromosome

Query Match 56.5%; Score 39; DB 2; Length 198;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAKFEAFKAA 11
||| |||:|
Db 95 KAKMEAFRAA 104

RESULT 13
A97405
hypothetical protein AGR_C_660 [imported] - Agrobacterium tumefaciens (strain C58, Cere
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C;Accession: A97405
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: A97405
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-217 <KUR>
A;Cross-references: UNIPROT:Q8UIC0; GB:AE007869; PIDN:AAK86194.1; PID:gl5155291; GSPDB:G
C;Genetics:
A;Gene: AGR_C_660
A;Map position: circular chromosome

Query Match 56.5%; Score 39; DB 2; Length 217;
Best Local Similarity 80.0%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 KAKFEAFKAA 11
||| |||:|
Db 114 KAKMEAFRAA 123

RESULT 14
T51971
proteasome endopeptidase complex (EC 3.4.25.1) chain PAD2 [imported] - Arabidopsis thali
N;Alternate names: 20S proteasome chain PAD2
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Oct-2000 #sequence_revision 20-Oct-2000 #text_change 09-Jul-2004
C;Accession: T51971
R;Fu, H.; Doelling, J.H.; Arendt, C.S.; Hochstrasser, M.; Vierstra, R.D.
Genetics 149, 677-692, 1998
A;Title: Molecular organization of the 20S proteasome gene family from Arabidopsis thali
A;Reference number: Z25275; MUID:9611183; PMID:9611183
A;Accession: T51971
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-250 <FUH>
A;Cross-references: UNIPROT:Q24616; EMBL:AF043523; PIDN:AAC32059.1
A;Experimental source: strain Columbia; seedling hypocotyls
C;Genetics:
A;Note: PAD2
C;Superfamily: multicatalytic endopeptidase complex chain C9
C;Keywords: hydrolase; proteinase

Query Match 56.5%; Score 39; DB 2; Length 250;

Best Local Similarity 76.9%; Pred. No. 40;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKFEAFKAAAAA 15
||| |||:|
Db 230 AKIEAEKAAAEA 242

RESULT 15

G87332

hypothetical protein CC0674 [imported] - Caulobacter crescentus

C;Species: Caulobacter crescentus

C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004

C;Accession: G87332

R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A;Title: Complete Genome Sequence of Caulobacter crescentus.

A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: G87332

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-389 <STO>

A;Cross-references: UNIPROT:Q9AAC8; GB:AE005673; NID:gl3421893; PIDN:AAK22659.1; GSPDB:G

C;Genetics:

A;Gene: CC0674

Query Match

Best Local Similarity 56.5%; Score 39; DB 2; Length 389;

Matches 9; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 2 KAKFEAFKAAAAA 15

||| |||:|
Db 66 KTSVETFKAAAPA 79

Search completed: March 31, 2005, 02:42:30

Job time : 18.9032 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:18:02 ; Search time 80.5645 Seconds
(without alignments)
95.342 Million cell updates/sec

Title: US-10-056-583A-95
Perfect score: 69
Sequence: 1 EKAKFEAFKAAAAA 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47.5	68.8	189	2 Q7M495	Q7m495 homarus ame
2	47.5	68.8	189	2 Q7M496	Q7m496 homarus ame
3	44	63.8	707	2 Q64CP3	Q64cp3 uncultured
4	43	62.3	99	2 Q6ERT5	Q6ert5 oryza sativ
5	43	62.3	299	1 RL22 DROME	P50887 drosophila
6	43	62.3	312	2 Q9UAN1	Q9uan1 drosophila
7	42	60.9	177	1 RL19 RHIME	Q92139 rhizobium m
8	42	60.9	179	1 RL19_AGR5	Q8ubz5 agrobacteri
9	42	60.9	181	1 RL19_RHILO	P58168 rhizobium l
10	42	60.9	274	2 Q6UK87	Q6uk87 burkholderi
11	42	60.9	386	2 Q6W1S9	Q6wls9 rhizobium s
12	42	60.9	395	2 Q6D7F3	Q6d7f3 erwinia car
13	42	60.9	508	2 Q6QUT5	Q6qt5 corynebacte
14	41	59.4	344	2 Q7QLQ4	Q7qlq4 anopheles g
15	41	59.4	346	2 Q9KR55	Q9kr55 vibrio chol
16	41	59.4	734	2 Q98KC4	Q98kc4 rhizobium l
17	41	59.4	828	2 Q9C6C7	Q9c6c7 arabidopsis
18	40	58.0	366	2 Q6FT73	Q6ft73 candida gla
19	40	58.0	369	2 Q65OY0	Q65oy0 oryza sativ
20	40	58.0	415	2 Q6YWS1	Q6yws1 oryza sativ
21	40	58.0	478	1 ATPB_RHOBL	P05440 rhodospseudo
22	40	58.0	614	2 Q64JV2	Q64jv2 plasmodium
23	40	58.0	698	2 Q44447	O44447 caenorhabdi
24	40	58.0	760	2 Q86A14	Q86a14 dictyosteli
25	40	58.0	3247	2 Q65553	Q65553 bovine herp
26	40	58.0	3247	2 Q77CD4	Q77cd4 bovine herp
27	39	56.5	41	2 Q84W05	Q84w05 arabidopsis
28	39	56.5	73	1 PHD_BPP1	Q06253 bacterioph
29	39	56.5	73	2 Q79A04	Q79a04 escherichia
30	39	56.5	113	2 Q19615	Q19615 caenorhabdi
31	39	56.5	144	2 Q9HX60	Q9hx60 pseudomonas

32	39	56.5	145	2 Q7Y3M5	Q7y3m5 enterobacte
33	39	56.5	153	2 Q7XVT5	Q7xvt5 oryza sativ
34	39	56.5	198	2 Q8UIC0	Q8uic0 agrobacteri
35	39	56.5	199	2 Q7W769	Q7w769 bordetella
36	39	56.5	217	2 Q7D1K6	Q7dlk6 agrobacteri
37	39	56.5	219	2 Q7WIK3	Q7wik3 bordetella
38	39	56.5	250	1 PS72 ARATH	Q24616 arabidopsis
39	39	56.5	273	2 Q72CN6	Q72cn6 desulfovibr
40	39	56.5	292	2 Q67PS1	Q67ps1 symbiobacte
41	39	56.5	300	2 Q9VFL4	Q9vfl4 drosophila
42	39	56.5	327	2 Q9XZR1	Q9xZR1 ciona intes
43	39	56.5	342	2 Q62L76	Q62l76 burkholderi
44	39	56.5	342	2 Q63V82	Q63v82 burkholderi
45	39	56.5	376	2 Q65WF6	Q65wf6 mannheimia

ALIGNMENTS

RESULT 1
Q7M495
ID Q7M495 PRELIMINARY; PRT; 189 AA.
AC Q7M495;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Exoskeletal protein HACP202B (Fragment).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL Submitted (JUN-1997) to the PIR data bank.
DR PIR; S77935; S77935.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 20180 MW; 72A4EFC9C7ECFE9 CRC64;

Query Match 68.8%; Score 47.5; DB 2; Length 189;
Best Local Similarity 75.0%; Pred. No. 6.2;
Matches 12; Conservative 2; Mismatches 1; Indels 1; Gaps 1;
QY 1 EKAK-FEAFKAAAAA 15
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DB 11 EKARFFQAFKAAEAAA 26

RESULT 2
Q7M496
ID Q7M496 PRELIMINARY; PRT; 189 AA.
AC Q7M496;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Exoskeletal protein HACP202A (Fragment).
OS Homarus americanus (American lobster).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;
OC Nephropoidea; Nephropidae; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP SEQUENCE.
RA Nousiainen M., Rafn K., Skou L., Roepstorff P., Andersen S.O.;
RL Submitted (JUN-1997) to the PIR data bank.
DR PIR; S77930; S77930.
FT NON_TER 1
FT NON_TER 189
SQ SEQUENCE 189 AA; 20154 MW; 72A4EFC9C647FE9 CRC64;
Query Match 68.8%; Score 47.5; DB 2; Length 189;

RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
RA Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
RA Lewis S.E.;
RT "Annotation of the Drosophila melanogaster euchromatic genome: a
RT systematic review.";
RT Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
RL [4]
RN SEQUENCE FROM N.A.
RP STRAIN=Oregon-R;
RC MEDLINE=20196011; PubMed=10731137; DOI=10.1126/science.287.5461.2220;
RX Benos P.V., Gatt M.K., Ashburner M., Murphy L., Harris D.,
RA Barréll B.G., Ferraz C., Vidal S., Brun C., Demailles J., Cadieu E.,
RA Dreano S., Gloux S., Lelaure V., Mottier S., Galibert F., Borkova D.,
RA Minana B., Kafatos F.C., Louis C., Siden-Kiamos I., Bolshakov S.,
RA Papagiannakis G., Spanos L., Cox S., Madueno E., de Pablos B.,
RA Modolell J., Peter A., Schoettler P., Werner M., Mourikioti F.,
RA Beinert N., Dowe G., Schaefer U., Jaekle H., Bucheton A.,
RA Callister D.M., Campbell L.A., Darlamitsou A., Henderson N.S.,
RA McWilliam P.J., Salles C., Tait E.A., Valenti P., Saunders R.D.C.,
RA Glover D.M.;
RT "From sequence to chromosome: the tip of the X chromosome of D.
RT melanogaster.";
RL Science 287:2220-2222(2000).
CC -!- SIMILARITY: Belongs to the ribosomal protein L22e family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; U42587; AAB17433.1; --
CC EMBL; AE003418; AAF45546.1; --
CC EMBL; AL132792; CAB60023.1; --
CC IntAct; P50887; --
CC FlyBase; FBgn0015288; Rpl22.
CC InterPro; IPR002671; Ribosomal_L22e.
CC Pfam; PF01776; Ribosomal_L22e; 1.
CC ProDom; PD007306; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT DOMAIN 24 31 Poly-Ala.
FT DOMAIN 46 50 Poly-Ala.
FT DOMAIN 65 70 Poly-Ala.
FT DOMAIN 93 98 Poly-Ala.
FT DOMAIN 103 112 Poly-Ala.
FT DOMAIN 136 152 Poly-Ala.
FT DOMAIN 185 188 Poly-Lys.
FT DOMAIN 292 299 Asp/Glu-rich (highly acidic).
SQ SEQUENCE 299 AA; 30610 MW; 46A99005610E4EB0 CRC64;

Query Match 62.3%; Score 43; DB 1; Length 299;
Best Local Similarity 73.3%; Pred. No. 52;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 36 EKPKAEAAKPAAAAA 50

RESULT 6
Q9UAN1 PRELIMINARY; PRT; 312 AA.
ID Q9UAN1
AC Q9UAN1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein L22 (Fragment).
GN Name=Rpl22; Synonyms=rpl22;
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99132306; PubMed=9931508; DOI=10.1016/S0378-1119(98)00529-0;
RA Koyama Y., Katagiri S., Hanai S., Uchida K., Miwa M.;
RT "Poly(ADP-ribose) polymerase interacts with novel Drosophila ribosomal
RT proteins, L22 and L23a, with unique histone-like amino-terminal
RT extensions.";
RL Gene 226:339-345(1999).
DR EMBL; AF080131; AAD19341.1; --
DR FlyBase; FBgn0015288; Rpl22.
DR GO; GO:0005622; C:intracellular; IEA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR002671; Ribosomal_L22e.
DR Pfam; PF01776; Ribosomal_L22e; 1.
KW Ribosomal protein.
FT NON_TER 1
SQ SEQUENCE 312 AA; 32273 MW; 0BE9A15CB473083B CRC64;

Query Match 62.3%; Score 43; DB 2; Length 312;
Best Local Similarity 73.3%; Pred. No. 55;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 49 EKPKAEAAKPAAAAA 63

RESULT 7
RL19_RHIME STANDARD; PRT; 177 AA.
ID RL19_RHIME
AC Q92L39;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rplS; OrderedLocusNames=R03246; ORFNames=SMC03863;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396507; PubMed=11481430; DOI=10.1073/pnas.161294398;
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,
RA Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
RA Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,
RA Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,
RA Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;
RT "Analysis of the chromosome sequence of the legume symbiont
RT Sinorhizobium meliloti strain 1021.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
CC interface and may play a role in the structure and function of the
CC aminoacyl-tRNA binding site (By similarity).
CC -!- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
CC EMBL; AL591793; CAC47825.1; --
CC HAMAP; MF_00402; -; 1.

DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMALL19.
DR ProDom; PD002979; Ribosomal_L19; 1.
DR TIGRFAMs; TIGR01024; rplS_bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 177 AA; 19255 MW; 1BD19D6561AB8F22 CRC64;

Query Match 60.9%; Score 42; DB 1; Length 177;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 136 EKARIEAEKVAAAAQ 150

RESULT 8
RL19_AGRTS
ID RL19_AGRTS STANDARD; PRT; 179 AA.
AC Q8UBZ5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rplS; OrderedLocusNames=Atu2703, AGR C 4900;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193; DOI=10.1126/science.1066804;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendinning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
RA Nester E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
C58.";
RL Science 294:2317-2323 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard C.,
RA Qurollo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaubin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328 (2001).
CC
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (By similarity).
CC
CC -!- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC
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CC
CC EMBL; AE009216; AAL43684.1; -.
CC

DR EMBL; AE008183; AAK88423.1; -.
DR PIR; AF2908; AF2908.
DR PIR; F97683; F97683.
DR HAMAP; MF_00402; -; 1.
DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMALL19.
DR ProDom; PD002979; Ribosomal_L19; 1.
DR TIGRFAMs; TIGR01024; rplS_bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 179 AA; 19474 MW; F3256BA44A5AD2D1 CRC64;

Query Match 60.9%; Score 42; DB 1; Length 179;
Best Local Similarity 66.7%; Pred. No. 48;
Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 137 EKARLEAEKVAAAAQ 151

RESULT 9
RL19_RHILO
ID RL19_RHILO STANDARD; PRT; 181 AA.
AC P58168;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE 50S ribosomal protein L19.
GN Name=rplS; OrderedLocusNames=mll4283;
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
Mesorhizobium loti.";
RL DNA Res. 7:331-338 (2000).
CC
CC -!- FUNCTION: This protein is located at the 30S-50S ribosomal subunit
interface and may play a role in the structure and function of the
aminoacyl-tRNA binding site (By similarity).
CC
CC -!- SIMILARITY: Belongs to the ribosomal protein L19P family.
CC
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CC
CC EMBL; AP003003; BAB50976.1; -.
DR HAMAP; MF_00402; -; 1.
DR InterPro; IPR001857; Ribosomal_L19.
DR Pfam; PF01245; Ribosomal_L19; 1.
DR PRINTS; PR00061; RIBOSOMALL19.
DR ProDom; PD002979; Ribosomal_L19; 1.
DR TIGRFAMs; TIGR01024; rplS_bact; 1.
DR PROSITE; PS01015; RIBOSOMAL_L19; 1.
KW Complete proteome; Ribosomal protein.
SQ SEQUENCE 181 AA; 19927 MW; AEF19D6593A9E835 CRC64;

Query Match 60.9%; Score 42; DB 1; Length 181;
Best Local Similarity 66.7%; Pred. No. 49;

Matches 10; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
Db 136 EKARIEAEKVAQA 150

RESULT 10

Q6UK87 PRELIMINARY; PRT; 274 AA.
AC Q6UK87;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gp64.
GN Name=ORF64;
OS Burkholderia cepacia phage Bcep43.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=260373;
RN [1]
RP SEQUENCE FROM N.A.
RA Summer E.J., Bomer M.L., Bean E.D., Embry A.E., Mebane L.M.,
RA Tsou L.L.-C., No E.-G., Gonzalez C.F., Young R.F.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY368235; AAR89355.1; -.
SQ SEQUENCE 274 AA; 28795 MW; 14419D38C3112965 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 274;
Best Local Similarity 71.4%; Pred. No. 71;
Matches 10; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 KAKFEAFKAAAAA 15
Db 116 KAEIEADKAAAAAS 129

RESULT 11

Q6W1S9 PRELIMINARY; PRT; 386 AA.
AC Q6W1S9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Spermidine/putrescine-binding protein.
GN ORFNames=NGR00516;
OS Rhizobium sp. (strain NGR234).
OG Plasmid megaplasmid 2.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=394;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGR234;
RA Broughton W.J., Perret X., Staehelin C., Schmitz R.A., Raasch C.,
RA Liesegang H., Gottschalk G., Streit W.R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY316747; AAQ87289.1; -.
DR HSSP; P31133; 1A99.
DR GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR006059; SBP_bac_1.
DR InterPro; IPR001188; Sperm/putr-bndng.
DR Pfam; PF01547; SBP_bac_1; 1.
DR PRINTS; PR00909; SPERMNDNDNG.
DR TIGRFAMS; TIGR01409; TAT_signal_seq; 1.
KW Plasmid.
SQ SEQUENCE 386 AA; 42194 MW; 5E56D6447B3B42F4 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 386;
Best Local Similarity 60.0%; Pred. No. 97;
Matches 9; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
Db 76 DPATFEAFKAAATGVA 90

RESULT 12

Q6D7F3 PRELIMINARY; PRT; 395 AA.
AC Q6D7F3;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Tola protein.
GN Name=tola; OrderedLocusNames=ECA1372;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebaihia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
RT "Genome sequence of the enterobacterial phytopathogen Erwinia
RT carotovora subsp. atroseptica and characterization of virulence
RT factors";
RL Proc. Natl. Acad. Sci. U.S.A. 101:11105-11110(2004).
DR EMBL; BX950851; CAG74282.1; -.
DR InterPro; IPR010528; Tola.
DR Pfam; PF06519; Tola; 1.
KW Complete proteome.
SQ SEQUENCE 395 AA; 41698 MW; 2DB1DAA64E984199 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 395;
Best Local Similarity 73.3%; Pred. No. 99;
Matches 11; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EKAKFEAFKAAAAA 15
Db 205 ETAKAEAAKAAAEAA 219

RESULT 13

Q6QUT5 PRELIMINARY; PRT; 508 AA.
AC Q6QUT5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE PS2.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=22243;
RX PubMed=15288952; DOI=10.1016/j.jbiotec.2004.03.020;
RA Hansmeier N., Bartels F.W., Ros R., Anselmetti D., Tauch A.,
RA Puhler A., Kalinowski J.;
RT "Classification of hyper-variable Corynebacterium glutamicum surface-
RT layer proteins by sequence analyses and atomic force microscopy.";
RL J. Biotechnol. 112:177-193(2004).
DR EMBL; AY525006; AAS20307.1; -.
SQ SEQUENCE 508 AA; 55416 MW; B28137E469228581 CRC64;

Query Match 60.9%; Score 42; DB 2; Length 508;

Best Local Similarity 60.0%; Pred. No. 1.2e+02; Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 EKAKFEAFKAAAAA 15
Db 104 EQAAYEAFEAARARA 118

RESULT 14
Q7QLQ4 PRELIMINARY; PRT; 344 AA.
AC Q7QLQ4;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Ebp455 (Fragment).
GN Name=ebiG455; ORFNames=ENSANGG00000000430;
OS Anopheles gambiae str. PEST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB01006298; EAA02717.1; --
DR GO; GO:0003998; F:acylphosphatase activity; IEA.
DR InterPro; IPR001792; Acylphosphatase.
DR InterPro; IPR001763; Rhodanese-like.
DR Pfam; PF00581; Rhodanese; 1.
DR PROSITE; PS50206; RHODANESE_3; 1.
FT NON TER 344 344
SQ SEQUENCE 344 AA; 39328 MW; C76C9D9A73D8B619 CRC64;

Query Match 59.4%; Score 41; DB 2; Length 344;
Best Local Similarity 75.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KFEAFKAAAAA 15
Db 75 KFEAFKAALFAS 86

RESULT 15
Q9KR55 PRELIMINARY; PRT; 346 AA.
AC Q9KR55;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Hypothetical protein VC1791.
GN OrderedLocusNames=VC1791;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1 Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";

RL Nature 406:477-483 (2000).
DR EMBL; AE004256; AAF94940.1; --.
DR PIR; C82156; C82156.
DR TIGR; VC1791; --.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 346 AA; 37684 MW; 8482E0264D91A6AA CRC64;

Query Match 59.4%; Score 41; DB 2; Length 346;
Best Local Similarity 90.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 EAFKAAAAA 15
Db 307 EAFKSAAAAA 316

Search completed: March 31, 2005, 02:41:13
Job time : 82.5645 secs